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June 27, 2002, 16:03:31 ; Search time 73.16 Seconds (without alignments) 215.589 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human insula	Mouse insulin fami	Mouse Zins3 protei	Pro-insulin-like	PRO182 polypeptide	human PRO182 prote Human insulin fami	PRO182 Polypeptide	Human PRO182 polyp
SUMMARIES	ID	AAG78114	AAW37926	AAW37925	AAY01961	AAB24391	AAY95770 AAY83228	AAM24033	AAU12309
	ngth DB	142 22	135 19	135 19	135 20	135 21	$\frac{135}{135}$ $\frac{21}{21}$	135 22	77
Query Match	raccii Lej	100.0 19.5	19.3	16.6 16.6	16.6	16.6	16.6	16.6	•
Score		760	126 5	126.5	126.5	126.5	126.5	126.5	
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Human immunostimul Sequence of human Amino acid sequence of porcin H2 prorelaxin gene Sequence of porcin H2 prorelaxin dedu Sequence of human Sequence of human Amino acid sequence Insulin like peptil human zins3 B chai Proleclaxin fragme Drosophila melanog Drosophila melanog Drosophila melanog Drosophila dinsi i Drosophila melanog Rat Zins2 testis-s Amgiotensish conver Protein. Unidenti Sequence encoded b Sequence of preprofiscili Human preproinsuli Human preproinsuli Human proinsulin Human Huma	ALIGNMENTS LT 1 8014 AAG780114 standard; Protein; 142 AA. AAG780114; 21-NOV-2001 (first entry) Human insulin homologue polypeptide Zins4. Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; heart disorder; vasotrophc; reproductive disorder; prostate disorder; heart disorder; kidney disorder; desticular cancer; carticular cancer; covarian syndrome; contractile tissue; cardiovascular disease; blirch control; impotence; movoyte; endothelial cell; osteoblast; blirch control; impotence; movoyte; endothelial cell; osteoblast; homo sapiens. (ev) Location/Qualifiers Homo sapiens. (ev) Location/Qualifiers Alabel= signal_peptide 2652 Alabel= B_chain (note= "Zins4, claimed in claim 4" 2652 Alabel= B_chain_consensus_sequence_region 34.47 Alabel= B_chain_consensus_sequence_region 37.41 /label= B_chain_conserved_motif
1110 100 100 100 100 100 100 100	Zins4 mosom ive dadal dadal dadal dadal dadal dadal dadal dadal dadal dadah naobhe iic be iic be iic be ii da in d
22 AAB20110 22 AAA053072 23 AAA0108 10 AAP94621 11 AAR07989 11 AAR07989 12 AAR07989 13 AAR040154 14 AAR079980 15 AAR040154 16 AAR040154 17 AAR040154 18 AAR040155 18 AAR040155 19 AAR040155 20 ABB62638 20 AAR0401963 21 AAR0401963 21 AAR0401963 22 AAR0401963 23 AAR0401963 24 AAR0401963 25 AAR0401963 26 AAR0401963 26 AAR0401963 27 AAR0401963 28 AAR0401963 38 AAR040193 38 AAR040194 38 A	ALIGNMENTS in; 142 AA. y) polypeptide Zins4. plaxin; chromosome 19 i; reproductive disort sorder; gonadal deve. sorder; gonadal deve. sorotractile tisst myocyte; endothelial chaln, comentic balanc lgnal_peptide ature_protein lns4, claimed in clain chain
222 222 222 222 222 222 222 222 222 22	142 in, eproper control on; lifting control on;
20000000400000000000000000000000000000	ntry) Le polype relaxin, ppic; repy disorder ause; repy drome; oc ce; myocy tension; tension; " Signal_ " " Signal_ " " B_chain " Claimed B_chain " Glaimed B_chain " Glaimed " Glacen in
135 135 135 136 136 137 137 137 137 137 137 137 137 137 137	ALIG. 114 standard; Protein; 142 AA. 14; -2001 (first entry) insulin; zins4; relaxin; chro rillity; vasotropic; reproduct disorder; kidney disorder; gon al change; menopause; ovarian stic ovarian syndrome; contrac; control; impotence; myocyte; er ressure; muscle tension; osmot piens. Location/Qualifiers 125 /label= signal_peptid 2614 2614 /label= mature_protei /label= mature_protei /label= mature_protei /label= mature_caime /label= B.chain /note= "Claimed in cla 3417 /label= B.chain_conser /note= "Given in SEQ 1 3741 /label= B.chain_conser
997477777777777777777777777777777777777	ard; Pr first e nomology zins4, vasotrc kidneg; kidneg; kingoten muscle nuscle 125 /label 2613 /label /note= 3447 /label /note= 3741
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1132 1144 1166 1176 1176 1176 1176 1176 1176	RESULT 1 AAG78114 STAC78114; AC AAG78114; AX 21-NOV-200 CX ALC78114; AX Human insu. CX AAG78114; AX Human insu. CX AAG78114; AX Human insu. CX AAG78114; CX
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/note= "Given in SEQ ID NO 5"
                                                              /note= "Given in SEQ ID NO 4"
                                              /label= A_chain
/note= "Claimed in claim 2"
                      "Claimed in claim 3"
                                                                                                                                                                 Claim 6; Page 72-73; 79pp; English.
                                                                                                                     Jaspers SR;
               'label= C_peptide
                                                                                           09-FEB-2001; 2001WO-US04199.
                                                                                                   10-MAR-2000; 2000US-0523346.
                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                       ..142
                                          119..142
           118
                          /note=
                                                                                                                      Holloway JL, Lok S,
                                                                                                                                                                                                                                                                                                             Sequence 142 AA;
                                                                                                                              WPI; 2001-582454/65.
                                                                                                                                   N-PSDB; AAH79088
                                                                          WO200168862-A1.
       Cleavage-site
                              Cleavage-site
                                                                                   20-SEP-2001
                                                          Region
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The present sequence is that of a murine paralog (see AAV95771) of munan zins3 (see AAY95770), a novel member of the insulin/relaxin cannot be munan zins3 (see AAY95770), a novel member of the insulin/relaxin cannot be made that more cannot be made a secondated family member that maps to a region of human chromosome la associated cannot be used converted to the sea of the sequence converted to the secondary of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                       61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDV 120
                           1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLGGREFIRAVIFTCGGSRWRRSDILAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%; Score 148; DB 21; Length 135; 29.9%; Pred. No. 2.8e-08; tive 21; Mismatches 51; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-insulin dependent diabetes mellitus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 46-47; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zins3; insulin; relaxin; mouse; NIDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY95771 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                           121 LAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                    10-FEB-2000; 2000WO-US03515.
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99US-0250125.
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Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-558220/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY95771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY95771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated insulin homologue zins4 having composition family. The zins4 gene, located on chromosome compositions as a lata amino acid protein, where the zins4 polypeptide 1913:11, encodes a 142 amino acid protein, where the zins4 bolypeptide comprises a B chain and A chain comprising amino acid residues 26-52 and comprises a betain and A chain comprising amino acid residues 26-52 and comprises a betain and A chain comprising amino acid residues 26-52 and comprises a betain a chain and a chain and vasotropic activity. Zins4 has cytostatic, antifertility and vasotropic activity. Zins4 polypeptides and in therapies for treating reproductive disorders. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the inhibitors of its activity. Zins4 polypeptides and modulators of the control of the zins4 polypeptides and modulators of the pathological conditions and other reproductive function, ovulation, prostate, testicular cancer, fertility, ovarian polypetides in the pathological conditions and other reproductive function associated conditions are also useful for treating dysfunction associated conditions and cancer. The molecules are also useful for treating dysfunction, with contractile tissues or to suppress or enhance contractility in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in culture and in the study of the ovarian cycle, reproductive function, ovarian cell-cell interactions and fertilisation. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic balance. The zins4 polynucleotide is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       birth control, treating impotence or other male reproductive dysfunction, inducing birth, for promoting growth, differentiation, development and/or maturation of overian cells, myocytes, endothelial cells, osteoblasts in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
                                                                                                                                                                                                                                                       /note= "Cleavage site at the junction of the C peptide and the A chain with a conserved RXXR motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 760; DB 22; Length 142; 100.0%; Pred. No. 1e-74; 0; Indels 0; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= A_chain_consensus_sequence_region
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Lok S;

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Gaps

0;

Best Local Similarity 100. Matches 142; Conservative

Query Match

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The Zins3 protein is an insulin homologue protein. Polynucleotide cusing an expression vector. The cell will express an insulin homologue cusing an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be conhuman animal. The polypeptides can be used to identify and isolate ceptors for zins3. Antibodies and antagonists of the polypeptides can ceptors for zins3. Antibodies and antagonists of the polypeptides can ceptors for zins3. Antibodies and antagonists of the polypeptides can cascotiated with the polypeptide, such as reproductive disorders.

C associated with the polypeptide, such as reproductive disorders can associated with the placenta and uterus, gastrointestinal diseases placental and colon pathology. Antagonists against the polypeptide may colon pathology. Antagonists against the polypeptide may colon pathology.
                                   61 EAMGDIFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                   Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                      Insulin homologue; identification; isolation; Zins3 receptor; treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lok S;
                                                                                  109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                Conklin DC, Jaspers SR, Lofton-Day CE,
                                                                                                                                                                     AAW37926 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /ucc.
49..115
"nte= "C-peptide"
                                                                                                                                                                                                                                                                                                                                                                    "B chain"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 67; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US18593.
                                                                                                                                                                                                                     01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                         23..48
/note=
                                                                                                                                                                                                                                               Mouse Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV29153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-1998.
                                                                                                                                                                                              AAW37926;
                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                           AAW37926
                                                                                                                                               RESULT
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135 AA;

Sequence

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The Zins3 protein is an insulin homologue protein. Polynucleotide

CC molecules taken from its gene can be introduced into a cultured cell

CC using an expression vector. The cell will express an insulin homologue

CC polypeptide encoded by the polynucleotide. The polypeptides can also be

CC combuman animal. The polypeptides can be used to identify and isolate

CC receptors for zins3. Antibodies and antagonists of the polypeptides can

CC receptors for zins3. Antibodies and antagonists of the polypeptides can

CC receptors for zins3. Antibodies any also be used in extracellular matrix and

CC sosciated with the polypeptide, such as reproductive disorders

CC associated with the placenta and uterus, gastrointestinal diseases, and

CC placental and colon pathology. Antagonists against the polypeptide may

CC also be used to treat diseases such as preclampsia, premature labour, and
                                          Gaps
                                                                                                     61 EAMGDTFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                                                                                             50 --lerhfhsqqaetrnylqlldrhepskktlehslpktdlsgqelvrdpqapkeg--lwe 105
                                                1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                   Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
              Length 135;
                                                                                                                                                                                                                                                                                                                                                            Insulin homologue; identification; isolation; Zins3 receptor;
treatment; disease; pre-elampsia; premature labour; Human.
                                      51; Indels
19.3%; Score 147; DB 19;
29.9%; Pred. No. 3.6e-08;
Conservative 21; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lok S;
                                                                                                                                                        109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                           106 1kkhsvvsrrd----lqalccregcsmkelstlc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jaspers SR, Lofton-Day CE,
                                                                                                                                                                                                                                                   AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 64-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "B chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "A chain"
                                                                                                                                                                                                                                                                                                       01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US18593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO ) ZYMOGENETICS INC.
           Similarity
                                                                                                                                                                                                                                                                                                                                   Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV29150
/ Mac
Local Sim.
46;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9816635-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1998.
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Query Match
                                                                                                                                                                                                                                                                              AAW37925;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                     Matches
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/label= Signal peptide
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                                                                                                                                                                                                                                                                        AAB00173 standard; Protein; 135 AA.
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99US-0144758.
99US-0145698.
99WO-US20594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0123957
                                                                                                                                                                                                                                                                                                                          08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                   Best Local Similarity 30.8
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                      130 KWGCSKSEISSLC 142
                                                                                                                                                                                                      ||| :::|:||
|123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                     PRO182 polypeptide.
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      135 AA;
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20-JUL-1999;
26-JUL-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                       AAB00173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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         Sequence
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                        RESULT (AABOO173
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                                                                                                                                                                                              δλ
x os
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an insulin-like polypeptide (pro-ILP).

CC The protein is expressed in the colon and uterus, and is a member cC of the insulin/GF family. The immature pro-ILP comprises a 135 amino cc acid sequence, which is processed into the mature form which comprises cC acid sequence, which is processed into the mature form which comprises cC and sequence, which is processed into the meture form which comprises of pro-ILP exists as a separate peptide after processing of pro-ILP. The exception is useful in treatment of disorders related to correct in treatment of disorders related to contropic activity, cardiovascular function, blood pressure, sommatic or cardiac homeostasis, cardiovascular function, blood pressure, sommatic or cardiac choncropic activity and collagen condition. The methods can be used for diagnosing a physiologic collagen condition of the uterus, colon or other ILP-expressing cell corrections and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                 Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac innotropic activity; cardiac chronotropic activity; cardiac chronotropic activity;
                                                                                                                                                               71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                       86 dasgedriwg-----gqmpteelwkskhsvmsrqd------iqtlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                 32 VRICGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDFFPDA 70
                                                                                                                                   39; Indels '45; Gaps
                                                               16.6%; Score 126.5; DB 19; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                    Pro-insulin-like peptide (pro-ILP).
                                                                                                                                                                                                                                                                                                             AAY01961 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Fig 6B; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US17888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0059836
                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999 (first entry)
                                                                                          Local Similarity 30.85 Local Similarity 30.85 Local Similarity
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                                                                                                                                                                                                                            130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                           ||| :::|:||
| 123 tdgcsmtdlsalc 135
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                                           135 AA;
                 Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09915664-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney A;
                                                                                                                                                                                                                                                                                                                                            AAY01961;
                                            Sequence
                                                                                 Query Match
                                                                                                          Matches
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86 dasgedriwg-----gqmpteelwkskkhsvmsrqd------iqtlcc 122
                                                                                                                                                                            71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                      32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                      Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; prostate cancer; lung cancer; bladder cancer; immunologic disorder; inflammatory disorder; angiogenic disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "CAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
16.6%; Score 126.5; DB 20; Length 135; 30.8%; Pred. No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Insulin family signature
125..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-myristoylation site"
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                                                      36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation site"
                                  30.8%; Preq. ... 8; Mismatches
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Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

or their agonists (preferably anti-PRO agonist antibody or a small

concleule minicking the biological activity of PRO polypeptide) are

compositions comprising the biological activity of PRO polypeptide) are

compositions comprising the PRO polypeptides are useful for temating neoplastic cell growth and for treating cancer including

contral nervous system cancer, unelanoma and leukaemia in a mammal.

con the PRO polypeptides are also useful for treating other disorders

con the PRO polypeptides are also useful for treating other disorders

con the PRO polypeptides are also useful for treating other disorders

con marcophagal, epithelial, strongial, hypothalamic and other glandular, astrocytal, lastococelic disorders as and

confirmmentory, anglogenic and immunologic disorders as well as being

consetul for identifying agonists to PRO polypeptides by contacting the artists and antity maniated by the activity maniated by contacting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
cytostatic; gene therapy; vaccine.
                                                                                                       Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, 'Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 dasgedriwg-----gampteelwkskkhsvmsrqd------1qtlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 vricgieyirtviyicassrwrrhlegipqaqqaetgnsfqiphkrefseenpaqnlpkv 85
                                                                                                                                                                                                           PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukeamia and for identifying compounds capable of inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%; Score 126.5; DB 21; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO182 protein sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                     Claim 31; Fig 10; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB24391 standard; Protein; 135 AA.
   99WO-US21090.
                      99WO-US23089.
                                        99WO-US28313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 30.88 hes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2000 (first entry)
                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                         WPI; 2000-638201/61.
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                                                                                                                                                                              N-PSDB; AAA54109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135 AA;
 15-SEP-1999;
                                  30-NOV-1999;
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing acardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The roughles caids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with anappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2438 represent nucleotide and protein sequences used in examplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                             Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or anglogenic disorders in mammals -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V Match
Local Similarity 30.8%; Pred. No. 6.1e-06;
hes 41; Conservative 8; Mismatches 39; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 dasgedriwg-----gqmpteelwkskkhsvmsrgd------iqtlcc 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                                                                                                                                                                                                                       Gerber H, Hillan KJ, Godda
Kuo SS, Paoni NF, Smith V;
                                                                                                                                                                                                                                                                                                                                                                                    Gerber H,
                                                                                                                                                                                                                                                                                                                                                                                     Asikenazi AJ, Baker KP, Ferrara N,
Godowski PJ, Gurney AL, Klein RD, F
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 72; Fig 8; 315pp; English.
                                                                                                                                                                                                                                                                                            99WO-US21547.
99WO-US23089.
99US-0162506.
                                              99WO-US28313.
                                                                                                                                                 99US-0131445.
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99US-0145698.
                                                                            98WO-US25108
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                                                                                                       99US-0115554
                                                                                                                                                                 99US-0134287
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                                                                                                                                                                                             99US-0141037
                                                                                                                                                                                                                                                                                99WO-US21090.
                                                                                                                                                                                                                                                                                                                                                                                  Baker KP,
Gurney AL,
                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KWGCSKSEISSLC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA77521.
                                          30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ,
               08-JUN-2000.
                                                                       01-DEC-1998
                                                                                                                                -MAR-1999;
                                                                                                                                                              14-MAY-1999
                                                                                                                                                                        02-JUN-1999
                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
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                                                                                                    12-JAN-
                                                                                                                                                 38-APR-
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||| :::|:|| 123 tdgcsmtdlsalc 135

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The present sequence is that of zins3, a novel member of the insulin/relaxin family. The zins3 gene maps to human chromosome to insulin/relaxin family. The zins3 gene maps to human chromosome (C insulin/relaxin family. The zins3 gene heritable form of non-linsulin dependent diabetes mellitus (MIDDM). Zins3 mRNA is not expressed in detectable amnounts in healthy tissue, indicating that the zins3 in detectable amnounts in healthy tissue, indicating that the zins3 polynucleotides and polypeptides can specialized cell type. Zins3 polynucleotides and polypeptides can be used to diagnose disorders associated with abnormal expression of the zins3 protein in the zins3 gene. In particular, the invention from mutations in the zins3 gene. In particular, the invention confirmation in the zins3 gene. In particular, the invention confirmation in the zins3 gene. In particular, the invention confirmation in glucose metabolism, such as NIDDM. Processing of the mature in glucose metabolism, such as NIDDM. Processing of the mature confirmation in involves cleavage at the C-terminus of the signal members of the insulin family, cleavage at the C-terminus of the remaining mand at the N-terminus of the A-chain, resulting in the N-mannial of the A-chain, resulting in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removal of the C-peptide. Cysteine residues at positions 29 and 41 (B-chain) and 121 and 121 and 135 (A-chain) are capable of associating through cysteine bridges and forming disulfide-bonded molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conklin DC, Lofton-Day CE,
                                                                                                                                                              Zins3; insulin; relaxin; human; diagnosis; NIIDM;
non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                        /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 44-45; 51pp; English.
                                                                                                                                Human insulin family homologue zins3.
                                                                                                                                                                                                                                                      Location/Qualifiers
                            AAY95770 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                       /label= C-chain
115..135
                                                                                                                                                                                                                                                                                                            23..48
/label= B-chain
                                                                                                                                                                                                                                                                                                                                                                                              /label= A-chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaspers SR, Whitmore TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                  07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-558220/51.
N-PSDB; AAA50150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200047776-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1999;
                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                   AAY95770;
                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                  Peptide
                    AAY95770
RESULT
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Composition for inhibiting neoplastic cell growth and treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein RD, Napier M, Wood WI;
                                                                           71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                86 dasgedriwg-----gqmpteelwkskkhsvmsrqd-------iqtlcc 122
                                                                                                                                                                                                                                                                                          Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182;
                               32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                     26 vrlogleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
             45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="cAMP and cGMP dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Insulin family signature sequence"
Best Local Similarity 30.8%; Pred. No. 6.1e-06;
Matches 41; Conservative 8; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-myristoylation site" 127...131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96..102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                      32..58 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi A, Goddard A, Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                         AAY83228 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US23089.
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125..13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              88..92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                130 KWGCSKSEISSLC 142
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123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-317943/27.
                                                                                                                                                                                                                                                                               PRO182 Polypeptide.
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                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                     AAY83228;
                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                         human.
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                                                                                                                                                                                             RESULT
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of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist
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                                                                                                                                                                                                                                                                                                                                                                          86 dasgedriwg-----gampteelwkskhsvmsrqd------iqtlcc 122
                                                                                                                                                                                                                 V Match 16.6%; Score 126.5; DB 21; Length 135; Local Similarity 30.8%; Pred. No. 6.1e-06; hes 41; Conservative 8; Mismatches 39; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                          71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                              32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH------EAMGDTFPDA 70
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26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpagnlpkv 85
                                                                         Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 by/Peptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qian XB, Wang Z, Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human EST encoded protein SEQ ID NO: 1558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 1068-1069; 1275pp; English.
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Cao Y, Drmanac RA, Zhang J, Werhman T;
                                           Claim 14; Figure 10; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM24033 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                                         130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                               123 tdgcsmtdlsalc 135
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                                                                                                                                                                         135 AA;
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                                                                                                                                                                       Sequence
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM24033;
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                          71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                    86 dasgedriwg-----gqmpteelwkskkhsvmsrqd-------1qtlcc 122
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                      32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH------EAMGDTFPDA 70
                                                                                                                                                                                                                               26 vrlcgleyirtviyicassrwrrhlegipgaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                  39; Indels 45;
                                                                                                                                                     16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred. No. 6.1e-06; Live 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                         AAU12309 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO182 polypeptide sequence.
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99WO-US28551.
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                                                                                                                                           Query Match
Best Local Similarity 30.8#
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US30999
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                                                                                                                                                                                                                                                                                                                                          123 tdgcsmtdlsalc 135
                                                                                                            135 AA;
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24-FEB-2000;
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ANULI72-AAU12446 represent novel human secretory and transmembrane

PRO polypeptides. The PRO polypeptides are useful to detect other

PRO polypeptides, to link bloactive molecules to cells expressing

PRO polypeptides, to modulate biological activities of cells expressing

PRO polypeptides, and to detect the presence of mammalian lung, colon,

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Dreast, prostate, rectal, cervical or liver tumours by comparing PRO

Common necrosis factor alpha (TMF-alpha) from human blood, the telease of

Common necrosis factor and the TMF-alpha from human blood, the comparing to a cartiflage, the proliferation of chondrocytes, the proliferation of funce are utricular supporting cells of

Cartiflage, the proliferation of inner ear utricular supporting cells of

Conf. 1-ymphocytes, the release of a cytchine from peripheral blood

Conf. 1-ymphocytes, the release of a cytchine from peripheral blood

Conf. 1-ymphocytes, the release of a cytchine from peripheral blood

Conf. 1-ymphocytes, the release of a cytchine from peripheral blood

Conf. 1-ymphocytes, the release of a cytchine from peripheral blood

Conf. 1-ymphocytes, the proliferation of endothelial cells. Some of

Conf. 1-ymphocytes, the proliferation of indicese fatty acid uptake by

Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide

Conf. 1-ymphocytes and be used to generate probes, antisense RNA/DNA,

PRO Polypeptides can be used to generate probes, antisense RNA/DNA,

Conf. 1-ymphocytes and produced and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
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                                                                                                                                                                                                             Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH------EAMGDTFPDA 70
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                                                                                                                                                                                                                                                                                                                                                                                         Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                          Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, G:
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 16.6%; Score 126.5; DB 22; Length Local Similarity 30.8%; Pred. No. 6.1e-06; nes 41; Conservative 8; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 dasgedrlwg----gqmpteelwkskkhsvmsrqd-----
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17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-UNN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.
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|123 tdgcsmtdlsalc 135
                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                              WPI; 2001-408281/43.
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                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS21381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB20110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The present sequence is that of PRO182 (UNQ156), a novel human commondulator protein encoded by CDNA (see AAF30052) isolated from a uterine cDNA library. The invention provides polynucleotides from a uterine cDNA library. The invention provides polynucleotides compositions comprising these proteins or including PRO182. Claimed compositions comprising these proteins or cells into a tissue of a mammal, stimulating or enhancing an immune crasponse in a mammal, or increasing the proliferation of Inflammatory crasponse in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising the PRO polypeptide or its antagonist have the opposite comprising the PRO polypeptide or its antagonist have the opposite comprising the PRO polypeptide or its antagonist have the opposite coup as a T cell disorder, involves administering the PRO polypeptide, such as a T cell disorder, involves administering the PRO polypeptide or treating an immune related disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, csteparthris, juvenile chronic arthritis, spondyloarthropathy, csteparthris, juvenile chronic arthritis, spondyloarthropathy, csteparthris, and inflammatory myopathy in csteparthris, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as immune-mediated colerosis), autoimmune chronic active hepatitis, primary commultiple sclerosis, grantlommune chronic active hepatitis, primary confliammatory bowel disease (ulcerative colitis and Crohn's disease), cf gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard A, Godowski PJ, Gurney AL;
Pitti RM, Tumas D, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                     107..111
/note= "cAMP- and cGMP-dependent protein kinase
PROJ82; UNQ156; human; immune disease; autoimmune disease; antirheumatic; antiarthritic; antiinflammatory; antianaemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiallergic; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "insulin family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                            /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation site"
                                                                                                                                                                                                                                                                                                         phosphorylation site'
                                                                                                                                                                                        1..18
/label= Signal_peptide
                                                                                                                                                                                                                                                /label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker KP, Fong S, G
Hillan KJ, Mark MR, Marsters SA,
                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 6; 127pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0144758.
                                                                                                                                                                                                                                                                                                                                                                                                                                               125..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121..136
                                                                                                                                                                                                                                                                                                                                                                                                       96..102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Allalmer's disease; Hutington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                              71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                                                                                                                                                                                                                                                     skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method activity of the PRO peptide, vectors, host cells and
                                                                                                                                                                                                                                                                    32 VRLCGREFIRAVIFTCGGSRWRR------SDILAH-----EAMGDTFPDA 70
                                                                                                                                                                                                                                                                                                26 vrlcgleyirtviyicassrwrrhlegipqaqqaetgnsfqlphkrefseenpaqnlpkv 85
                                                                                                                                                                                                                                             45;
                                                                                                                                                                                                         16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred. No. 6.1e-06; Live 8; Mismatches 39; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human angiogenesis-associated protein PRO182, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB53072 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; transgenic animal.
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99WO-US28565.
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                                                                                                                                                                                                                                          41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    123 tdgcsmtdlsalc 135
                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                 Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200053753-A2
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02-DEC-1999;
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                                                                                                                                     antibodies
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                                                                                                                                                                                                            Query Match
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PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, acrdiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as a therosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, chooses, wounds, cancer, Alzheimer's disease, Hutington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential
                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel human anglogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, description of a PRO protein, agonists or antagonists of a PRO protein, additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder with the administration of a PRO protein.
                                                              Goddard A;
ark MR, Marsters SA;
                                                                                                                                                                                                                           New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or anglogenic disorders, such as atherosclerosis, wounds or cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.6%; Score 126.5; DB 22; Length 135; 30.8%; Pred. No. 6.1e-06; tive 8; Mismatches 39; Indels 45;
                                                                     KP, Ferrara N, Gerber H, Goddard A,
AL, Hillan KJ, Kuo SS, Mark MR, Ma
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 dasgedrlwg-----gqmpteelwkskkhsvmsrqd-----
                                                                                                                                                                                                                                                                                                                         Claim 69; Fig 18; 293pp; English.
                                                                   Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 KWGCSKSEISSLC 142
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123 tdgcsmtdlsalc 135
                                                  Ashkenazi AJ, Baker
1.1 p.T, Gurney
                                                                                                                   Pitti RM,
                                                                                                                                                            WPI; 2001-090793/10.
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                                                                                                                                                                                    N-PSDB; AAC97396
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                                                                                                                   Paoni NF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAP40108 standard; Protein; 185 AA.

AAP40108

AAP40108;

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           AAP94621
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim a ds DNA SQ which comprises a coding strand and a complementary strand corresp. to (AAN40086) and its subunits. Also claimed are synthetic human H2-preprorelaxin, human H2-prorelaxin and human H2-relaxin together with their analogues having shortened A or B chains, or modified to contain different AA residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| : | |: : : : | ||::| || 61 dapgnprpvaelvpsfinkdtetinmmsefvanlpgelkltlsemgpalpglgghvpvlk 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 -----AFYRGRPS-----WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MARYMLLLLLAVWVLTGELWPGAEARAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA-----LIKS-----PQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene for expression of human H2-preprorelaxin – useful as vector for prodn. of the peptide after expression etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 111.5; DB 5; Length 185; 22.7%; Pred. No. 0.00038; ive 23; Mismatches 77; Indels 43;
                                                                Relaxin; hormone; probe; uterine contraction.
                                                                                                                  Location/Qualifiers
                                      Sequence of human preprorelaxin H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tregear GW;
                                                                                                                                                                                58..161
/label= C-peptide
162..185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 56pp; English.
                                                                                                                                                         25..57
/label= B-chain
                                                                                                                                                                                                           162..185
/label= A-chain
                                                                                                                                              /label= signal
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HOWARD FLOREY INST.
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             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.73
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hudson PJ, Niall HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1984-160129/26.
N-PSDB; AAN40086.
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larfc 185
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01-JAN-1988;
            04-FEB-1992
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                                                                                                                                                          Region
                                                                                                                                                                                   Region
                                                                                                                                                                                                             Region
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"H2" relaxin is deduced from a cDNA clone, has the general properties of a growth factor and is capable of altering nature of connective tissue and inducing smooth muscle contraction, specifically during labour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 dapqtprpvaeivpsfinkdtetinmmsefvanlpgelkltlsemqpalpglqqhvpvlk 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 ------AFYRGRPS------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKS-----PQ------ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human H2-relaxin analogues - with shortened and/or modified A and/or B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.4%; Score 109.5; DB 1
Best Local Similarity 22.7%; Pred. No. 0.00062;
Matches 42; Conservative 22; Mismatches 78
                                                                                                                                 Amino acid sequence of human preprorelaxin H2.
                                                                                                                                                                                                                                                                                       1..25
/label=Signal peptide
                                                                                                                                                                             Relaxin; H2-relaxin; pubic symphysis.
                                                                                                                                                                                                                                                                Location/Qualifiers
AAP94621 standard; protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                /label=B-chain
58..161
/label=C-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hudson PJ, Trgear GW, Niall HD;
                                                                                                                                                                                                                                                                                                                                                                                                                   162..159
/label=A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83EP-0110103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82AU-0007247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FLOR-) FLOREY H INST EXPER.
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 AA;
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                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1982;
                                                                                     21-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP303033-A.
                                              AAP94621;
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                                                                                                                                                                                                                                                                                                                                                                            Peptide
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4;

0.7 0.7 0.7 0.7

Search completed: June 27, 2002, 16:08:08 Job time: 277 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

June 27, 2002, 16:05:31; Search time 28.78 Seconds (without alignments) 120.515 Million cell updates/sec Run on:

US-09-781-077-2 760 1 MARYMLLLLIAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142 Perfect score: Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628 seqs, 24425594 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		pesci iprion	Sequence 6, Appli	Sequence 2, Appli	Patent No. 5464756	Sequence 12, Appl	Patent No. 5464756	ž	ž	ce 1	10,	10,	14	92,	12,	12,	2.7	,	7	Sequence 11, Appl	~	7	7	Sequence 2, Appli	7	4	13,	13,	٠,
SUMMERTES	£		US-08-950-720A-6	US-08-950-720A-2	5464756-16	US-08-950-720A-12	5464756-18	5464756-20	5464756-15	US-08-950-720A-13	US-08-443-568B-10	PCT-US94-06997-10	US-08-950-720A-14	US-08-353-476-92	US-08-443-568B-12	PCT-US94-06997-12	US-09-201-226-2	US-08-905-267-2	US-09-314-051-2	US-08-950-720A-11	US-08-589-028-2	US-08-784-582-2	US-08-785-271-2	PCT-US95-08596-2	US-08-697-954-2	US-08-484-219-4	US-08-905-267-13	US-09-314-051-13	5464756-8
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æ	Query			16.6	15.3	14.4	14.1	13.5	13.4	13.0	12.9	12.9	12.5	12.2	11.8	11.8	11.6	11.6	11.6	11.1	11.1	11.1	11.1	11.1	10.5	10.0	10.0	10.0	8.6
	Score		148	126.5	116	109.5	107.5	102.5	102	98.5	86	86	95	92.5	89.5	89.5	88.5	88.5	88.5	84.5	84.5	84.5	84.5	84.5	79.5	92	92	7	74.5
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Patent No. 5464756	Patent No. 5464756	Sequence 19, Appl	Sequence 19, Appl	Sequence 19, Appl	Sequence 4, Appli	4	4	Sequence 2, Appli	5	Sequence 2, Appli	90,	14,	14,	28,		Sequence 12, Appl	12,
5464756-11	5464756-10	US-08-911-853-19	US-09-479-409-19	US-09-479-453-19	US-08-589-028-4	US-08-784-582-4	US-08-785-271-4	US-08-443-568B-2	US-08-484-219-5	PCT-US94-06997-2	US-08-353-476-90	US-08-443-568B-14	PCT-US94-06997-14	US-07-989-845-28	US-07-989-844-12	US-08-161-044-12	US-08-240-121-12
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32	33	174	174	174	110	110	110	59	58	53	33	52	52	94	94	94	94
9.6	9.6	9.5	9.5	9.5	9.4	9.4	9.4	9.3	9.3	9.3	9.3	9.3	6.9	9.1	9.1	9.1	9.1
73	73	72	72	72	71.5	71.5	71.5	71	71	7.1	71	71	7.1	69	69	69	69
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSSTEME OF Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                          APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOWOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/950,720A
                   ; Sequence 6, Application US/08950720A; Patent No. 6046028; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sawislar, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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                                                                                                                                                                                                                                                                                                                           98102
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US-08-950-720A-6
                                                                                                                                                                                                                                                                                   STATE: WA
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Query Match

19.5%; Score 148; DB 3; Length 135;

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71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                             86 DASGEDRLWG-----LGOMPTEELWKSKKHSVWSRQD------LGTLCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                               Patent No. 5464756

Patent No. 5464756

Patent No. 1990 DENNIS J.; VANDLEN, RICHARD L.; WILKINS, JAMES A.; YANSURA, DANIEL G.

TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE J. ISOLATION HUMAN RELAXIN

NUMBER OF SEQUENCE: 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.3%; Score 116; DB 6;
86.4%; Pred. No. 8.8e-07;
tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SUSTWARRE: FASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GIKLCGREFIRAVIYTCGGSRW 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 GVRLCGREFIRAVIFTCGGSRW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                      130 KWGCSKSEISSLC 142
                                                                                                                               123 TDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 30
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                                                                                                                                                 61 EAMGDIFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                                                                                                                                             : | | : | | | : 50 -- LEGHFHSQQAETRNYLQLLDRHEPSKKTLEHSLPKTDLSGQELVRDPQAPKEG--LWE 105
                                                                                           1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
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                          51; Indels
    29.9%; Pred. No. 1.3e-09; ive 21; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720a
                                                                                                                                                                                                                                   109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 VRLCGREFIRAVIFTCGGSRWRR-----
                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08950720A
Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 30.8
Matches 41; Conservative
                          46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 120-
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                             US-08-950-720A-2
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Gaps ; 0

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                                                                                                                                                                                                                                                                                                                                                                                                 121 DSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDTHSRKKRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                                              78; Indels 43; Gaps
                                                                                                                                                                                                                                               1 MARYMLLLLLAVWYLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                     61 EAMCDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKS-----PQ------98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 14.1%; Score 107.5; DB 6; Length 162;
Local Similarity 23.4%; Pred. No. 7.6e-05;
hes 36; Conservative 20; Mismatches 55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 A-----LTKS-----PQ------WQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ANLPQELKLTLSEMQPALPQLQOHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADBDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 109.5; DB 3; Length 185; 22.7%; Pred. No. 5.3e-05; tive 22; Mismatches 78; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.;VANDLEN, RICHARD L.;WILKINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                         INFORMATION FOR SEQ ID NO: 12:
                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046028e
US-08-950-720A-12
                                        SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
                                                                                                                                                                                                                  42; Conservative
TELEFAX: 206-442-6678
                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOLATION HUMAN RELAXIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA.
                                                                              amino acid
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ISSLC 142
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9 IKLCGRELVRAQIAICGMSTWSKRSLDSQEDAPQTPRPVAEIVPSFINKDTETINNMSEF 68
                                                                                                                                                                                                                                                                                                                                                          32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDT------FPDADADEDSLAGEL 81
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                                                                                                                                                                                                                                                                                     ch 13.5%; Score 102.5; DB 6; Length 164; 1 Similarity 22.4%; Pred. No. 0.00029; 35; Conservative 20; Mismatches 56; Indels 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,
S A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAMES A., YANGGRA, DANYEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 QGTPGVLRGSRDVL-AGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LGLDTHSRKKRDQLYSALANKCCHVGCTKRSLARFC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NAMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                          APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-UU-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CONKlin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/08950720A; Patent No. 6046028; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZymoGenetics, Inc.
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                                . ISOLATION HUMAN RELAXIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                   Best Local Similarity
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Best Local Similarity
JAMES A.; YANSURA,
                                                                                                                                                                                                           ; LENGTH: 164
5464756-20
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; Patent No. 5464756
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                                                                                                                                                                                        ; SEQ ID NO:20:
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 DAPOTPRPVABIVPSFINKDTETIIIMLEFIANLPPELKAALSERQPSLPELOQYVPALK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 KSPQAF-----YRGRPS------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 13.0%; Score 98.5; DB 3; Length 185;
Local Similarity 23.8%; Pred. No. 0.00098;
nes 44; Conservative 19; Mismatches 79; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MARYMLLLLLAUWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
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APPLICANT: Breece, Kirk
APPLICANT: Hayonga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
APPLICANT: Poniel, Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    OPERATING SYSTEM: DOS
SORTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08443568B Patent No. 5759807 GENERAL INFORMATION:
                      1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEPAX: 206-442-6678
TELEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear _
MOLECULE TYPE: No. 6046028e
                                                                                                                                                                                                                                                                                                                                                               NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,4
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                Seattle
                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                      FILING DATE:
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STATE:
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                                STREET:
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Matches
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12.9%; Score 98; DB 1; Length 77;
19.8%; Pred. No. 0.00035;
Live 14; Mismatches 23; Indels 52; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application Pc/TUS9406997
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
APPLICANT: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
  COMPUTER READBLE FORM:
COMPUTER. ISPA PC Compatible
COMPUTER: ISPA PC Compatible
COMPUTER: SYSTEM: PC-DOS/WS-DOS
COFFWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.8%; Pred. No. 0.000
Matches 22; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Damoine STREET: 1155 Avenue of the Americas
                                                                                                             CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22-MAY-1995
FILING DATE: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             PILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/080,354
PILING DATE: 21-JUNE-1993
CLASSIFICATION NUMBER: 08/080,354
ATTORNEY/AGENT INFORMATION:
NAME: ADDRAGN: Samuel B.
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennie & Edmonds
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ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3'
CORRESPONDENCE ADDRESS:
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U.S.A.
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10036
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Gaps

us-09-781-077-2.rai

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33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA 92
                                                                                                                                                                       Gaps
                                                                                                                                                                                                            93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                               ch 12.5%; Score 95; DB 3; Length 101; 24; Conservative 14; Mismatches 30; Indels
                                                                                                                                                                                                                                       65 ----PQTSHHH------RHHRAAATNPAKYCCLSGCTQQDLLILC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%; Score 92.5; DB 2; Length 40; 52.9%; Pred. No. 0.00065; Indels 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Weininger, Susan
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
NUMBER OF SEQUENCES: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PNWEERS-----RLCGRDLIRAFIYLCGGTRWTR 30
                                                                                                                                                                                                                                                                                                             Sequence 92, Application US/08353476
Patent No. 5871902
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REPRENCE/DOCKEN NUMBER: GP-1C
TELEBOOMUNICATION INFORMATION:
TELEBAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 40 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity.
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                   US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32606
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US-08-353-476-92
                                                                                                                                                                                                                                                                                                 US-08-353-476-92
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                 RESULT 12
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                                                                                                                                                                                                                                                                       23; Indels 52; Gaps
                                                                                                                                                                                                                                                                               32 VRLCGREFIRAVIFICGGSRWRRSDILAHEAMGDIFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                    92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                               th 12.9%; Score 98; DB 5; Length 77; 15.8%; Pred. No. 0.00035; 22; Conservative 14; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                    7842-025-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
ITLE OF INVENTION: INSULIN HOMOLOG
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-84-360
TELEPAX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid acids
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: ZymoGenetics, Inc.: 1201 Eastlake Avenue East
Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08950720A
Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REMABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: No. 6046028e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 101 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                            Query Match
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; Sequence 12, Application US/08443568B

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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THILD OF THE TREFERENCE: 7326-077
THIE REFERENCE: 7326-077
CURRENT APPLICATION NUMBER: US/09/201,226
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 VLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | : : |: || || :: || 121 HSRKRQLYSALANKCCHVGCTKRSLARFC 150
                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854.3660
TELEPHONE: 415-854.3694
                                                                                                                                                                                       CT/US94/06997
20-JUN-1994
N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-201-226-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-201-226-2
Sequence 2, Application US/09201226
Patent No. 6135942
                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-854-3694
TELEE: 66141 PENNIE
INFORMATION FOR SED ID NO: 12:
SEQUENCE CHARACTERIZICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%
Query Match
Best Local Similarity 25.5%
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 amino acids
                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein pcT-US94-06997-12
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                              New York
                                                                  U.S.A.
                                                                                                                                                                                                                                               CLASSIFICATION:
                                New York
                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                    10036
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GRELVRAQIAICGMSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFVANLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.7%; Pred. No. 0.008;
Matches 34; Conservative 18; Mismatches 55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 GREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA--- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for producing Relaxin
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/443.568R PILING NAMES.
                                                                                                                                Process for Producing Relaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 VLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application PC/TUS9406997
GENERAL INFORMATION:
                                                                                                                                                                                               F: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7842-037
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORBY disk
MEDIUM TYPE: FLORBY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIVE
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 7842-
REFERENCE/DOCKET NUMBER: 7842-
TELECOMMUNICATION INFORMATION: 650-493-5556
TELERAX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acids
                                            APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Rindersknecht, Ernst
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION 435
PRIOR APPLICATION DATA: 08/080,354
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Abrams, Samuel B. REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-443-568B-12
                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                  U.S.A.
                                        GENERAL INFORMATION:
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                      Patent No. 5759807
                                                                                                                                                                                                                                                                                                  10036
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                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                               STREET:
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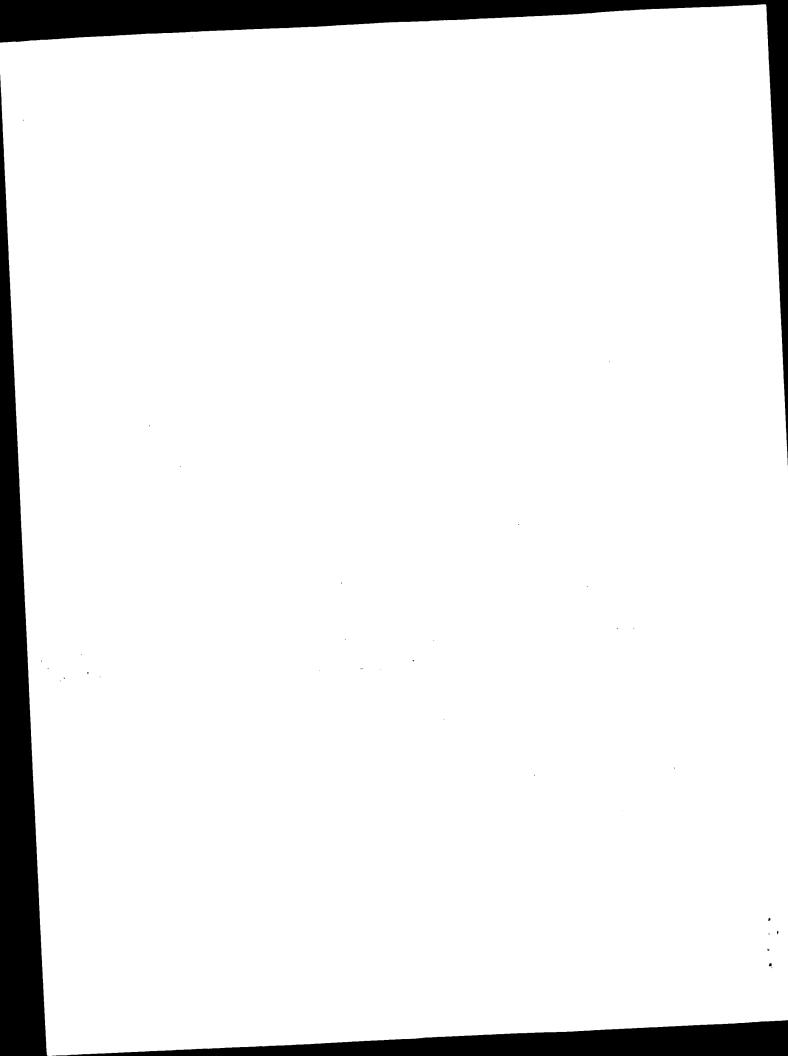
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25.5%; Pred. No. 0.009; 4; Indels 29; Gaps
tive 19; Mismatches 60; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 ----LTKS------PQ-------WQGTPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QELKLTLSEMQPALPQLQQHVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GRELVRAQIAICGMSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFVANLP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 GREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA--- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leptin, Maria
APPLICANT: Leptin, Maria
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF A D. MELANOGASTER
TITLE OF INVENTION: NUCLEIC ACIDS AND USES THEREOF
TITLE OF INVENTION: INSULIN-LIKE GENE AND USES THEREOF
TITLE OF INVENTION: 1326-077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%; Score 89.5; DB 5; Length 150; 22.7%; Pred. No. 0.008; 55; Indels 43tive 18; Mismatches 55; Indels 43
        3: Pennie & Edmonds
1155 Avenue of the Americas
CORRESPONDENCE ADDRESS:
```

us-09-781-077-2.rai

Page 7

Search completed: June 27, 2002, 16:08:44 Job time: 193 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2002, 16:05:56; Search time 36.01 Seconds (without alignments) 378.914 Million cell updates/sec Run on:

1 MARYMLLLLLAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142 US-09-781-077-2 760 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		١	1	relaxin 2 precurso	N	Dr		relaxin precursor	a	•–	relaxin precursor		relaxin precursor		•	insulin-related nr	ocrill	tei	Ξ.			insulin precursor	conserved hypothet	insulin-like growt	relaxin - minke wh			S I	pitstinamycin I sy	fxbC protein - Mrs	Frocetti
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dР	Query	20.1	15.4	14.4	7.7	14.0		•		•	13.0	13.0	12.9	12.6		•	•	11.	11:	11:1	0.01	10.5	10.	10.0		•		5.0	10.3	10.1	10.1	
	Score	153	117	109.5	108.5	106.5	102	101.5	100.5	66	66	98.5	86	95.5	89.5		86.5	9 6	84.5	83.5		80.5		80	8.		; -	0 0	0 1	77	11	
,	Result No.		7	æ	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	22	÷ (970	7	

peptide synthetase relaxin - horse (final in precursor conserved hypothet transcription regultranscription regultranscription regultypothetical prote conserved hypothetical prote probable zinc meta probable zinc meta probable zinc meta catalase (EC 1.11. relaxin - Bryde's insulin precursor insulin precursor	TOSTING INTERCIT PORT NO.
714164 A49739 A49739 A439883 IPHF C83171 FGECAY FGECAY FGECAY FGECAY C975349 A53697 A53697 A53697 A53697 A11PCH A1	
000000000000000	
2569 48 108 1115 380 513 513 513 513 667 576 54 109	
10.1 10.1 10.1 10.1 10.0 10.0 10.0 9.9 9.9 9.9	
77 76.5 76.5 76.5 76.5 76.5 76.5 74.5 73.5 73.5 73.5	
331 331 331 444 544 55	

ALIGNMENTS

RESULT A26463 C; Spec C; Spec C; Acce R; Bull Bur. J Bull Bur. J A; Titl A; Resid A; Molec A; Molec B; Bxper C; Keywor C; Keywor C; Keywor C; Keywor F; 1-30, F; 1-30, F; 1-30, F; 1-30, F; 1-30,	RESULT 1 A26463 relaxin - spiny dogfish (fragments) C;Species: Squalus acanthias (spiny dogfish) C;Accession: B26463 A26463 R;Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, A./Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (sq. A./Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (sq. A./Accession: B26463 A./Accession: B26463 A./Accession: B26463 A./Accession: B26463 A./Accession: B26463 A./Accession: B26463 A./Accession: B26403 A./Accession: B26403 A./Accession: B26403 A./Accession: A26463 A./Ac
Quea Bess Matc Qy Db Oy Oy	Ouery Match 20.1%; Score 153; DB 2; Length 54; Best Local Similarity 28.6%; Pred No. 5.2e-08; Matches 32; Conservative 10; Mismatches 4; Indels 66; Gaps 2; 31 GVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDAADEDSLAGELDEAMGSSEW 90 9 GIKLCGREFIRAVITATCGGSR
RESULT RXRKOT relaxi. C; Spec C; Date C; Acce: R; Gowal F; Gowal A; Title A; Title A; Refes	RESULT 2 RETROT RETROT C.SPECIES: Odontaspis taurus (sand tiger) R.Sowan, L.K.; Reinig, J.W.; Schwabe, C.; Bedarkar, S.; Blundell, T.L. FEBS Lett. 129, 80-82, 1981 A.Fitler On the primary and tertiary structure of relaxin from the sand tiger shark A.Reference number: A01616 A.Accession: A01616

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A, Residues: 1-182 <-HEL>
B, James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
B, James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
Nature 267, 544-546, 1977
A, Title: Primary structure of porcine relaxin: homology with insulin and related grow A, Title: Primary structure of porcine relaxin: homology with insulin and related grow A, Title: Primary structure of porcine relaxin: homology with insulin and related grow A, Reference number: A93187, MUID:77213067
A, Reference number: A93187
A, Reference number: A93187
A, Residues: 25-50, TWGR'; 161-182 <-JAM>
A, Residues: 25-50, TWGR'; 161-182 <-JAM>
A, Residues: 25-50, TWGR'; 161-182 <-JAM>
A, Schwabe, C.; McDonald, J.K.; Steinetz, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relaxin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: O2-Apr.1982 #sequence_revision 02-Apr.1982 #text_change 18-Jun-1999
C;Dates: 02-Apr.1982 #sequence_revision 02-Apr.1985; S32312; A29796; A01615
C;Accession: A90934; A93187; A90205; A90196; S32313; S32312; A29796; A01615
R;Haley, J.; Hudson, P.; Scanlon, D.; John, M.; Cronk, M.; Shine, J.; Tregear, G.; Ni
DNA 1, 155-162, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ANLPOELKLTLSEMOPALPOLOOYVPVLKDSSLLFEEFKKLJRNROSEAADSSPSELKYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pan troglodytes (chimpanzee)
C;Species: Ob-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: Z27245; NID: 9416109; PIDN: CAA81758.1; PID: 9416110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 IKLCGRELVRAQIALCGKSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFV 72
                                                                                                                                                                                               121 DSSLLFEEFKKLIRNRQSEAADSSPSELKYLGLDTHSRKKRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                61 DAPQTPRPVAEIVPSFINKDTETINMMSEFVANLPQELKLTLSEMQPALPQLQQHVPVLK 120
                                                                                                                                 ------AFYRGRPS------WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSE 137
61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA-----LIKS-----PQ----- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 A-----LTKS-----PQ-------AFYRGRPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Porcine relaxin: molecular cloning and cDNA structure. A;Reference number: A90934; MUID:83157118
A;Accession: A90934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: insulin
C;Superfamily: signal sequence (fragment) #status predicted <SIG>
F;1-5/Domain: signal sequence (fragment) #status predicted <MAT>
F;6-166/Product: relaxin 2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 108.5; DB 2; Length 1 darity 23.4%; Pred. No. 0.0031; Conservative 20; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relaxin 2 precursor - chimpanzee (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S42776
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Best Local Similarity
Matches 36; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: S42786
R; Evans, B.B.
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                                                                                                                                                                                                                                                                                                    138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                     181 LARFC 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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A, Residues: 25-53;162-185 <STU>
C; Genetics:
C; Genetics:
C; Genetics:
C; Genetics:
A, Gene: GDB:RLN2
A, Cones postition: 9pter-9q12
A, Cross-references: GDB:I1953; OMIM:179740
A, Map position: 9pter-9q12
C; Superfamily: insulin
C; Keywords: ovary: pyroglutamic acid
F; 25-53, 162-186, Product: relaxin 2 #status experimental <ACH>
F; 25-53, 162-186, Product: relaxin 2 chain A #status experimental <ACH>
F; 162-186, Domain: relaxin 2 chain A #status experimental <ACH>
F; 162-186, Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X00948; NID:g35926; PIDN:CAA25460.1; PID:g35927
R;Stults, J.T.; Bourell, J.G.; Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow, J.W. Biomed. Brointon. Mass Spectrom. 19, 655-664, 1990
A;Title: Structural characterization by mass spectrometry of native and recombinant huma A;Reference number: A60982; MUID:91167739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: preprorelaxin 2
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A05092; A60982
C;Accession: A05092; A60982
B;Hudson, P; John, M; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear EMBO 13, 2333-2339, 1984
A;Fitle: Relaxin gene expression in human ovaries and the predicted structure of a human A;Feference number: A05092; MUID:85051298
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1;2-19;21-44 <GOW>
A; Residues: 1;2-19;21-44 <GOW>
A; Residues: 1;2-19;21-44 <GOW
A; Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.P.
Bur. J. Blochem. 161, 335-341, 1986
A; Title: Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalue, Reference number: A91179; MUID: 87054035
A; Reference number: A91179; MUID: 87054035
                                                                                                                                                                                                             A; Contents: annotation; sequence revision
A; Contents: annotation; sequence revision
A; Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
A; Note: the carboxyl-terminal sequence of chain B was determined to be Arg-Trp
C; Reywords: pyroglutamic acid
C; Reywords: pyroglutamic acid
C; Reywords: pyroglutamic acid
F; 1.47 Domain: chain B (fragments) #status experimental
F; 1.47 Domain: chain A #status experimental
F; 1.47 Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 3-31,15-44,30-35/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ------PAMSIKGCIYGGTKKDISVLC 44,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 15.4%; Score 117; DB 1; Local Similarity 24.5%; Pred. No. 0.00013; hes 27; Conservative 6; Mismatches 11:
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Matches 42; Conservative
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A; Residues: 1-185 <HUD>
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NiAlternate names: Ley I-L
C; Species: Sus scrofa domestica (domestic pig)
C;Date: 03-May-1994 *sequence_revision 03-May-1994 *text_change 05-Nov-1999
C;Accession: A53024; A49687
R;Burkhardt, E; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattei, M.G.; Engel, W.
Genomics 20, 13-19, 1994
A;Title: Structural organization of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral organization of the porcine and human genes coding for a Leydig chiral organization of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the porcine and human genes coding for a Leydig chiral procession of the procession of the porcine and human genes coding for a Leydig chiral procession of the procession of the porcine and human genes coding for a Leydig chiral procession of the procession of t
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J. Biol. Chem. 268, 26668-26672, 1993
A.Title: Cloning of a CDNA for a novel insulin-like peptide of the testicular Leydig A; Accession: A49687; MUID:94075362
A; Molecule type: mRNA
A; Residues: 1-131 < ADH>
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C; Species: Macaca mulatta (rhesus macaque)
C; Species: Macaca mulatta (rhesus macaque)
C; Species: May 34936 #sequence_revision 07-Sep-1990 #text_change 12-Jun-1998
R; Crawford, R.J.; Hammond, V.E.; Roche, P.J.; Johnston, P.D.; Tregear, G.W.
J. Mol. Endocrinol. 3, 169-174, 1989
A; Title: Structure of rhesus monkey relaxin predicted by analysis of the single-copy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:25-56/Domain: Leydig insulin-like protein chain B #status predicted <BCH>F:57-105/Domain: connecting C peptide #status predicted <CPEP>F:106-131/Domain: Leydig insulin-like protein chain A #status predicted <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: GB:X58369
A.Experimental source: testis
A.Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
C.Genetics:
A.Gene: INSL3
A.Map position: 19913.2-p12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ELL---OWLEGOHLFHGLMASGDPMLVLAPOPPPQAS-GHHHHRRAAATNPARHCCLSGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: DNA
A;Residues: 1-131 <BUR>
A;Cross-references: GB:X73636; NID:g871548; PIDN:CAA52016.1; PID:g871549
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                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: A53024
A, Status: preliminary; not compared with conceptual translation
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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-185/Product: relaxin #status predicted <MAT>
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                                                              Leydig insulin-like protein precursor - pig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TRODLLTLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-185 <CRA>
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A:Reference numbers. Angel Auguston and Auguston Angel Auguston Angel Auguston and Angel Auguston and Angel Auguston Angel Ange
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PAETMPSSITKDAEILKMMLEFVPNLPQELKATLSER-----OPSLRELQQSASKDSNLN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 -----GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 FEEFKKIILURQNEAEDKSLLELKNLGLDKHSRKRRLFRWTLSEKCCQVGCIRKDIARLC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LLAVWYLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LLGVWLLLSQLPREIPGGSTNDFIKACGRELVRLMVEICGSVSWGRTALSLEEPQLETGP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 106.5; DB 1; Length 182; 21.7%; Pred. No. 0.0053; Live 22; Mismatches 68; Indels 51;
                                                A; Title: Primary structure of the B-chain of porcine relaxin.
A; Reference number: A90205; MUID:77157271
A; Accession: A90205
Biochem. Biophys. Res. Commun. 75, 503-510, 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Conservative
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13.4%; Score 101.5; DB 2; Length 185; 22.7%; Pred. No. 0.016; itive 22; Mismatches 78; Indels 43; Gaps

Query Match
Best Local Similarity 22.7:
Matches 42; Conservative

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C:Species: Mas muscules (house mouse)
C:Species: Mas musculus (house mouse)
C:Date: O'7. May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C:Jaccession: S48082; Pc2067; PN0626
C:Accession: S48082; Pc2067; PN0626
C:Accession: B.A.; John, M.; Fowler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear, J. Mol. Endocrinol. 10, 15-23, 1993
J. Mol. Endocrinol. 10, 15-23, 1993
A;Title: The mouse relaxin gene: nucleotide sequence and expression.
A;Reference number: S48082; MUD:93199663
A;Accession: S48082; MUD:93199663
A;Accession: S48082
A;Accession: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 R-----RSDILAHEA--MGDTFPDADAD------EDSLAGELDEAMGSSEWLA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARYMLLLLLAVWVL-----TGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Indels 56; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 EWLA------LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 OWLERRHLLHGLVADSNLTLGP-----GLQPLPQTSHHHRHHRAAATNPARYCCLSGCTO 122
                                                                                                                                                                                                                                                                                                                                                                                            37; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 RLCGREFIRAVIFTCGGSRW----RRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB:S72482; NID:9632798; PIDN:AAB31371.1; PID:9632799 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.7%; Pred. No. 0.029;
Matches 47; Conservative 20; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.2%; Pred. No. 0.02;
Matches 32; Conservative 12; Mismatches 37; Indels
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F;13-57/Domain: chain B #status experimental <CHA>
F;161-185/Domain: chain A #status experimental <CHA>
F;36-171,48-185,170-175/Disulfide bonds: #status experimental
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                                                                                                                                                    A; Cross-references: GDB:230307; OMIM:146738
                                                                                                                                                                                        A; Map position: 19p13.2-19p12
A; Introns: 64/1
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A; Residues: 161-185 <BU2>
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A; Molecule type: mRNA
A; Residues: 1-131 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 SEISSLC 142
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                                                                                                                                      A; Gene: GDB: INSL3
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R;Burkhardt, E.; Adham, I.M.; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
Hum. Genet. 94, 91-94, 1994
A;Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
A;Reference number: I54278; MUID:94307715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Raja erinacea (little skate)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 IDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISS 140
                                                                                                                                                                                                                                               61 DAPLKPRPAAEIVPSLINQDTETINMMSEEVANLPQELKLTLSERQPALSELQQHVPVLK 120
                                                                                                                                                                                                                                                                                                                                                               121 DSNLSFEEFKKIIRKRQSBATDSSPSELRSLGLDTHSRRKRQLYMTLSNKCCHIGCTKKS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGE 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 MEEKM-----GFAKKCCAIGCSTEDFRM 62
                                                                                                                                                                                                                                                                                                                       98 ------QAFYRGRPS--WQGTPGVLRG------SRDVLAGLSSSCCKWGCSKSE 137
                                                                                          1 MARYMLLLLLAVWVLTGELWPGAEARAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                 61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKSP------ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K;Bullesbach, E.E.; Schwabe, C.; Callard, I.P.
Biochem. Biophys. Res. Commun. 143, 273-280, 1987
A;Title: Relaxin from an oviparous species, the skate (Raja erinacea).
A;Reference number: A29543; WUID:87156758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 100.5; DB 2; Length 64; 22.1%; Pred. No. 0.0071; tye 11; Mismatches 25; Indels 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-64 <BUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LAKFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 LC 142
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63 VC 64
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93	,
Db 114 HAPVLSDSVVSLEGFKKTLHDRLGEAEDGSPPGLKYLQSDTHSRKRESGGLMSOOCCHV 173	פווכם דבא דא ז
	K;Hudson, P.; Haley, J.; Cronk, M.; Shine, J.; Niall, H. Nature 291, 127-131, 1981
Db 174 GCSRRSIAKL 183	A:Title: Molecular cloning and characterization of cDNA sequences coding for rat relar, A:According to the part of
RESULT 11	A. Molecule type: mRNA A. Molecule type: mRNA A. Boeidhoe: 1-106
A44559 relaxin 1 precursor - human	A/Crossidudes: 1.160 ABUD> A/Crossidudes: 1.160 ABUD> A/Crossidudes: 1.160 ABUD ABUD ABUD ABUD ABUD ABUD ABUD ABUD
N;Alternate names: prepredatin 1 C;Species: Homo sapiens (man)	C: Keyertaning: . insulin C: Keyertaning: . bormone; ovary; pyroglutamic acid F:1-22/Domain: circa) . companing:
C;Date: 03-Feb-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999 C;Accession: B05092; A44559	F.23-57/Domain: signar Sequence #Status predicted <sig>F.23-57/Domain: relaxin chain B #status predicted <krb>F.23-57,163-186/Product relaxin #status predicted <krb></krb></krb></sig>
R; Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tregear EMBO J. 3, 2333-2339, 1984	F:58-162/Domain: relaxin connecting pedicted <pre>F:163-186/Domain: relaxin chain A #status modited .status predicted <rxc></rxc></pre>
A. Title: Relaxin gene expression in human ovaries and the predicted structure of a human A. Reference number: A05092; MUID:85051298 A. Reference number: A05092; MUID:85051298	F;36-173,48-186,172-177_minified bonds: *status predicted F;163/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predi
A: Molecule type: DNA A: Residues: 1-185 <ht></ht>	CHOT Match
A; Cross-references: GB:X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933 R; Hudson, P.; Haley, J.; John, M.; Cronk, M.; Crank, M.; Cronk, M.; Cr	Similarity 12.3%; Score 98; DB 1; Length 186; Similarity 23.8%; Pred No. 0.036; Conservative 75. Mismatch.
Nature 301, 628-631, 1983 A:Title: Structure of a genomic clone encoding biologismis.	LILLAVWVITGETADEARAADVVVVITGETATA
A; Reference number: A44559; MUID:83141755 AAccession: A44559	
A; Molecule type: DNA A; Residues: 1-185 <hu2></hu2>	
	28
distille Donds.	
A;Gene: GDB:RLN1 A;Cross-references: GDB:119552; OMIM:179730	118 PALSDSVVSLEGFRKTFHNOLGBARDAGDPRIVICARAGEDERGEDERGEDERGEDERGEGERGEGERGEGERGE
A; Map position: 9pter-9q12 C; Superfamily: insulin	Qy 134 SKSEISSIC 142
C; Keywords: hormone; ovary F: 1-25/Domain: signal sommone attentions.	170
F;26-57,20main: sigual Sequence status predicted <sig> F:26-57,20main: relaxin 1 chain B #status predicted <bch></bch></sig>	
F:58-158/Domain: relaxin 1 connecting C peptide #status predicted <pre>CP:58-158/Domain: relaxin 1 connecting C peptide #status predicted <cpep></cpep></pre>	RESULT 13
F;35-172,47-185,171-176/Disulfide bonds: #status predicted <ach></ach>	relation 1 precursor - chimpanzee (fragment)
Ollows Matak	C.becles: Pan troglodytes (chimpanzee) C.bate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text change 16-15,1000
Best Matches 13.0%; Score 98.5; DB 1; Length 185; Matches 44: Concernation 10.0032;	C:Accession: S42783 R:Evensis, B.B. Ribmaitted to the pure net out
Ov 1 Made Matternation of the Machine Color of Machine Color S;	A:Reference number: S42776
Db 1 MPRIELEHHILTEROILTIANDERRAYAANTAARAANTAAAAAAAAAAAAAAAAAAAAAAAAA	A.Accession: S42/83 A.Molecule type: mrNA A.Residine: 1-166 - rux
Qy 61 EAMGDTPPDADADPENCE:	A:Constants 100 CEVAL
61 DAPQTPRPVAEIVPSFINKDTETIIIMLEPIANLPPEIRAALSRPOPSTEDFOOOVIDS	A/Gene: Tix1 C/Superfamily: insulin
٠ .	C; Keywords: disulfide bond; hormone F;1-5/Domain: signal sequence (frament) #status and sequence (frament)
Db 121 DSNLSFEEFKKLIRNRQSEAADSNPSELKYLGLDTHSQKRRRPYVALFRKCC1.1GCTRFS 190	F;6-166/Product: relaxin 1 #status predicted <amt></amt>
QY 138 ISSLC 142	Query Match 12.6%; Score 95.5; DB 2: Iength 166.
Db 181 LAKYC 185	Pred. No. 0.056; ; Mismatches 55; Indels
RESULT 12	75
RXRT relaxin precursor - rat	Db 13 IKLCGRELVRAQIAICGMSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETIIIMLEFI 72
	QY 76 -SLAGELDEAMGSSEWLALTKSPQAFYRGRPS 106
	<u>:</u> -

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Gaps

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 67-116 < HIE>
A; Residues: 67-116 < HIE>
A; Residues: 67-116 < HIE>
Bur. J. Blochem. 201, 495-499, 1991
Bur. J. Blochem. 201, 495-499, 1991
A; Title: Isolation and structural characterization of an insulin-related molecule, A; Reference number: S17851; MUID: 92037603
A; Molecule type: protein
A; Residues: 34-64,123-143 < HET>
C; Genetics: 34-64,123-143 < HET>
C; Genetics: 70/1
F; 1-22/Domain: siqual sequence #status predicted < SIG>
F; 34-64/Product: insulin-related protein chain B #status experimental < BCH>
F; 67-116/Product: connecting peptide #status experimental < PEP>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
F; 123-143/Product: insulin-related protein chain A #status experimental < ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 AHEAMGDIFPDADADEDSLAGELDEAMGSSEWLALIKSPQAFYRGRPSWQGTPGVLRGS- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 FKKASQDV-SDSESEDNYWSGQSADEAAEAAAALPPYP---ILARPS---AGGLLTGAV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LILLLAVWVLT----GELWPGAEARA-APYGV-RLCGREFIRAVIFTCGGSRWRRSDIL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 88; DB 2; Length 145; 26.7%; Pred. No. 0.26; Live 28; Mismatches 59; Indels
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A; Reference number: S07773; MUID: 90126826
A; Accession: S07773
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A;Cross-references: EMBL: 229963
B;Laqueux, M.; Lwoff, L.; Meister, M.; Goltzene, F.; Hoffmann, J.A.
Eur. J. Biochem. 187, 249-254, 1990
A;Title: cDNAs from neurosecretory cells of brains of Locusta migratoria (Insecta, Orthd A;Reference number: S07774; MUID: 90126827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kromer-Metzger, E.; Lagueux, M.
Eur. J. Biochem. 221, 427-431, 1994
A;Title: Expression of the gene encoding an insulin-related peptide in Locusta (Insecta, A;Reference number: S43124; MUID:94222089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)tCross.references: EMBL:X170247. RID:99529; PID:99530 R; Hoffmann, J.; Luu, B. R; Hietter, H.; van Dorsselaer, A.; Green, B.; Denoroy, L.; Hoffmann, J.; Luu, B. Eur. J. Blochem. 187, 241-247, 1990 A; Title: Isolation and structure elucidation of a novel 5-kDa peptide from neurohaemal
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C;Date: 28-Sep-1994 #sequence_revision 12-Apr-1996 #text_change 12-Jun-1998
C;Accession: S43224; S07774; S07773; S17851; S42153
                                                                                                                                                                                                                                                                                                       c.species: Canis lupus familiaris (dog)
C.Species: Canis lupus familiaris (dog)
C.Species: Cape-1994 # sequence_revision 26-May-1995 #text_change 26-May-1995
C.Sacession: B53879; A53879
R.Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. protein Chem. 11, 247-253, 1992
A;Fille: Purification and sequence determination of canine relaxin.
A;Reference number: A53879; MUID:93000391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LKACGRDYVRLQIEVCGSSWWGRK------35
                          73 ANLPPELKAAL--SERQPSLPEPQQYVPALKDSNLSFEEFKKLIRNRQSEAADSNPSELK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DNYIKMSDKCCNVGCTRRELASRC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 89.5; DB 2; Length 59; 20.7%; Pred. No. 0.075; tive 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: placenta
A; Note: sequence extracted from NCBI backbone (NCBIP:115401)
A; Accession: A53879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Nore: sequence extracted from NCBI backbone (NCBIP:115399) C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-35,36-59/Product: relaxin #status experimental <MAT>F;1-35,70cmain: chain B #status experimental <CHB>F;36-59/Domain: chain A #status experimental <CHB>F;36-59/Domain: chain A #status experimental <CHA>F;9-46,21-59,45-50/Disulfide bonds: #status predicted
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                                                                                                                                   107 WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
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A; Residues: 1-131,'T',133-145 <LAG>
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Best Local Similarity 20.7%
Matches 23; Conservative
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A; Residues: 1-35 <STE>
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A; Residues: 36-59 <ST2>
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A; Residues: 1-145 <KRO>
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2002, 16:08:11; Search time 58.57 Seconds (without alignments) 419.417 Million cell updates/sec Run on:

US-09-781-077-2

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

562222 seqs, 172994929 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_vertebrate:*
sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_mhc:*
sp_organelle:*
sp_phage:* sp_rvirus:*
sp_bacteriap:* 1: sp_archea:* 2: sp_bacteria:* sp_plant:*
sp_rodent:*
sp_virus:* sp_archeap:* sp_mammal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	;	qi	3 Q9DEP8	Q9MYK8	610N60	09GK47	8±0N60	0.000 0.000	973055	CAMH6O	21 HILLS	057687	D24890			09KZR1	054959	009209	
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	1 S	052999 agrobacteri 053649 mycobacteri 006075 mycobacteri 0944M6 drosophila	Q98ta7 osteoglossu 095082 homo sapien 09p0v3 homo sapien 09f0d7 streptomyce 028431 gorilla gor 092xb0 rhisohium m	772045 mycobacteri Q939y9 amycolatops Q9406 oryza sativ Q83380 rat leukemi Q99pll corcyra cep	O9ZIX3 pseudomonas Q91gc0 oryza sativ Q91tc2 arabidopsis Q67939 hepatitis b Q67938 hepatitis b
2 11 11 11	4 09UPH6 2 09LA28 16 09RTD1 2 09SOR7	16 16 13	44791	9 00	10 09LGC0 10 09LFC2 12 067939 12 067938
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 DSNLNLEEVEKSILGRQNEAEDQSLSQLGRSRLDAHSRIKRSDYIRYSDRCCNVGCTRKE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 LAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL-----ALTKSPQAFYRGRPSWQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARYMLLLLLAVWVLTGELWPGAEARAAPYG----VRLCGREFIRAVIFTCGGSRWRRSDI 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Gaps
                                61 RSNPNRDFLDWLNRASLEDPDRLNSLYAESHMAPNPPFSSLQKDDPTMEQLHGALYDPLV 120
55 ----SDIL-----BEANGDTFPDADADE---DSLAGELDEAMG 86
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99115216; PubMed-9915995;
MEDLINE-99115216; PubMed-Klonisch S., Froehlich C., Kauffold J.,
Klonisch T., Huppertz B., Fischer B.;
Steger K., Huppertz B., Fischer B.;
"Nucleic acid sequence of feline preprorelaxin and its localization
                                                                 87 SSEWLALTKSPQAFYRGRPSWQGTPGV-LRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                   121 TEE-----QQGVGLRMKRS--AGPALSCCQRGCTKNELMKFC 155
                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Hombach-Klonisch S., Klonisch T.;

Hombach-Klonisch S., Klonisch T.;

Hombach-Klonisch S., Klonisch T.;

-1- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro: IPK, 0000739; Insulin_IGF_relaxin.
SMART: SM00078; I1GF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               within the feline placenta.";
Biol. Reprod. 60:305-311(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF233688; AAF60303.1; --
HSSP; P04090; 6RLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 LADLC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREPRORELAXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                     RELAXIN.
                                                                                                                                                                                                Q9MYK8
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Q9N0T9
                                                                                                                                                                   RESULT
                                                                                                                                                                                   Q9MYK8
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Klonisch T., Froehlich C., Tetens F., Fischer B., Hombach-Klonisch S., "Molecular remodeling of members of the relaxin family during primate evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 13.3%; Score 101; DB 6; Length 131;
Best Local Similarity 24.5%; Pred. No. 0.01;
Matches 39; Conservative 15; Mismatches 45; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ERQPSAEPQQPALKDSNLNFEEFKKIIFDRQNBEEDESLSELKNLGLDKHSEK----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PRPAPKPALRPALSQDKKPRLRSGPPAEIMPSSITKDAETLTTMLEFTPNLPQELTATLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 DTFPDADADEDSLAG-------ELDEAMGSSEWLALTKSPQAFYRGRPS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPRLLISHLIGVWLLISQLPKETSGERSNDFVKACGRELVRLWIEICGSVSWGRPAPRPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 -----AMG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRR----- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
Camelus dromedarius (Dromedary) (Arabian camel).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
                                                                                                               MEDLINE-20191540; PubMed=10727251; MEDLINE-20191540; PubMed=10727251; Mediane-Klonisch 7. Abd-Elnaeim M., Skidmore J.A., Leiser R., Fischer B., Klonisch T.; Ruminant relaxin in the pregnant one-humped camel."; Ruminant relaxin in the pregnant one-humped camel."; Biol. Reprod. 62:839-846(2000).

-: SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).

-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL, APE24139; AAF67741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    13.6%; Score 103.5; DB 6; Length 199; 18.1%; Pred. No. 0.0096; tive 24; Mismatches 62; Indels 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOI. Biol. Evol. 0:0-0(2001).
-i- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317624; AAG42317.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; INSULIN; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;
                                                                                                                                                                                                                                                                         HSSP; P01348; IRLX.
InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00708; IJGF, INSULIN: 1.
PROSTIE: PS00262; INSULIN: 1.
SEQUENCE 199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 WQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELAXIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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53 ----PEAGT---SSAGGDRELL---OWLERPHLLHGLVAEHDPALVPGLQPLPQASHHH 101
                                                               -----ALTKSPQAFYRG 103
                 |:|| || || || 5 LSVWALVLLGPALVFALHPSLSLETRE---KLCGHHFVRALVRLCGGPRWS----- 52
10 LAVW--VLTG-----ELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 E--LDEAMGSSE---WLALTKSPQA--FYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDS---LAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra hirous (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 12.9%; Score 98; DB 6; Length 131; Best Local Similarity 27.7%; Pred. No. 0.021; Matches 36; Conservative 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 131 AA; 14406 MW; EC7731679E60B0C7 CRC64;
                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                         102 -----RHHRAATINPAHRCCLSGCTRQDLLTLC 129
                                                                                                          104 RPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                              131 AA.
                                                      63 MGDTFPDADADEDSLAGELDEAMGSSEWL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 131 AA.
                                                                                                                                                                                                                                                                                     Dama dama (Fallow deer) (Cervus dama).
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                          PRELIMINARY;
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NCBI_TaxID=9925;
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                                                                                                                                                                                                                                                                         RELAXIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 CSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 CTRODLLTLC 129
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=30532;
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O9NOT8
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 δ
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Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 EAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLR--GSRDVLAGLSSS------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AEARAAFYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AAAQEAP--EKLCGHHSVRALVRLCGGPRW-----51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ----SGRPVAGGDRELLRWLEGQHLLHGLMASGDPVLVLAPQPLP 95
                                                            Hombach-Klonisch S., Tetens F., Kauffold J., Steger K., Flscher B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klonisch T.; "Molecular cloning and localization of caprine relaxin-like factor (RLF) mRNA within the goat testis."; Mol. Reprod. Dev. 53:135-141(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                        TISSUE-TESTIS;
Hombach-Klonisch S., Klonisch T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
'- SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF233686; AAF60301.1;
                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 88; DB 6; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
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--- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317625; AAG42318.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 86; DB 6; Length 188;
                                                                                                                                                                                                                                                                  Interpro; IPR000739; Insulin_iGF_relaxin.
Pfan; PF00049; Insulin; 1.
PROSTIE; PS00206; INSULIN; 1.
PROSTIE; PS00206; INSULIN; 1.
SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 188 AA; 21573 MW; 77551629B82B9A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.6%; Score 88; DB 6;
Best Local Similarity 21.4%; Pred. No. 0.22;
Matches 33; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 QASRHHHRRATAINPARHCCLSGCTRQDLLTLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.3%; Pred. ms.
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TISSUE-EMBRYONIC TROPHOBLAST, PLACENTA;
                              TISSUE=TESTIS;
MEDLINE=99260294; PubMed=10331451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.3% hes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
               SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM N.A.
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Matches
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01-JUN-1998 (TrEMBLrel. 06, Created)
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                                                                                                                                                                                                                                                                               InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 2.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00138; SUBTILASE_SER; 1.
                                                                                                                                                                                                                                            Genômê Res. 8:135-145(1998).
EMBL; AL356713; CAB92392.1; -.
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POSSIBLE SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1601 DETRFORDYAA 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GVLRGSRDVLA 122
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                                                                              SEQUENCE FROM N.A.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=72052;
                                                                                                                                                                                                                                                                        MEROPS; SOB.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holzenberger M.;
                                                     NCBI_TaxID=5664;
                                                                                             STRAIN-FRIEDLIN;
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057687
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STRAIN—ARCC 15692 / PAO1;
MEDLINE=20437337, PubMed=10984043;
MEDLINE=20437337, PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 ------LDTAEEAAAWTRLAQVRRKALFGASLPAWIGVPGVFAGLNGVALI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 TFPDADADEDSLAGELDEAMGSSEW--LALIKSPQAFYRGRPSWQGTPGV---LRGSRDV 120
                                                                                    107 EMNLPSPELQQYPPTLKGSDISFEEVKNNIHNEQGEAEDNSHSELQNLGLDTHSRKKRER 166
                                                                    52 WRRSDILAH-----EAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGD 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LLPLILVEFFLGELQPLPHGLAMPLFIAALLSMFVNLPLF----GAYKRGLIATQKA--- 74
                                  1 MARYMLLLLLAVWVLTGELWPGAEARA-APYGVRL-----CGREFIRAVIFTCG--GSR 51
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.0%; Pred. No. 0.83;
Matches 34; Conservative 14; Mismatches 56; Indels 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE004821; AAC07433.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 139 AA; 15161 MW; 9F5D69D2981A389A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                       01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1722 AA.
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                            104 R-----PSWOGTPGVLRGS------
                                                                                                                                                                                121 LAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                          167 YMSPLOKCCRIGCTKRSLARFC 188
                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN PA4046.
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                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeroidea; Passeridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Indels 44; Gaps
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Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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Holzenberger M., Jarvis E.D., Chang C., Grossman M., Nottebohm F.,
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Selective expression of insulin-like growth factor II in the song
bird brain.";
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oliver K., Harris D., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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Last annotation update)
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Nucleotide sequence and genomic structure of the chicken insulin-like growth factor-II (IGF-II) coding region.";
Gen. Comp. Endocrinol. 102:383-287(1996).";
-I-SUMCELLUIAR LOCATION: SECRETED (BY SIMILARITY).
EMBL: 882962; AAB46818.1;
-EMBL: 882966; AAB46818.1;
-HSSP: P01344; IGF2.
                                                                                                                                                                                                                                                                                                                                                                                                    60 HEAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TIENBLE-1. 03, Last sequence update)
01-DEC-2001 (TIENBLE-1. 19, Last annotation update)
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                           64; Gaps
                                                                                                                                                                                                                                                                                                                                       2 ARYMLLLLLLAVWYLTGELWPGAEARAAPYGV--RLCGREFIRAVIFTCGGSRWRRSDILA 59
                                                                                                                                                                                                                                                                                                                                                                4 ARRMLILLIAFLAY------AMDSAAAYGTAETLCGGELVDTLQFVCG--------45
                                                                                                                                                                                                                                                                                                                                                                                                                                    46 ------GRINNRR 61
J. Neurosci. 17:6974-6987(1997).

-I. SUBGELLULAR LOCATION: SECRETED (BY SIMILARITY).

EMBL; AJ23165; CAAJ1145.1; -

INSEP; PO1344; 1GF2.

Interpro; IPRO00799; Insulin, I.

PRINTS; PRO0276; INSULINA.

PRINTS; PRO0276; INSULINA.

PRODOM; POD01048; Insulin, I.

PRINTS; PRO0276; INSULINA.

PRODOM; POD01048; Insulin, I.

PRODOM; POD01048; Insulin.

PRODOM; POD01048; Insulin.

PRODOM; POD01048; Insulin.

PRODOM; POD01048; Insulin.

PROPOM; POD01048; Insulin.

PROPOM; POD01048; Insulin.
                                                                                                                                                                                                                                                                                  10.5%; Score 80; DB 13; Length 187; 23.1%; Pred. No. 2.1; tive 8; Mismatches 38; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.5%: Score 80; DB 13; Length 187;
Best Local Similarity 22.4%; Pred. No. 2.1;
Matches 32; Conservative 10; Mismatches 37; Indels
                                                                                                                                                                                                                  CHAIN 24 187 IGF-II PRECURSOR.
SEQUENCE 187 AA; 20908 MW; 3C7EADA8F7D2CE8F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 AA.
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PROMOST, INSULINA.
PRODOM: PD010404; INSULINB.
SMART; SM00078; INSULIN.
PROSITE: PS00262; INSULIN; 1.
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                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 VLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 FNRGIVEECCFRSCDLALLETYC 84
                                                                                                                                                    SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 23.18
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00049; Insulin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 AA;
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                                                                                                                                                                                       Signal.
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P79890
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EMBL; AB010693; BAB10876.1;

InterPro; IPR001584; Rve.

InterPro; IPR001584; Znf_CCHC.
                                                                                                                        60 HEAMGDTFPDADADEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
NCBI_TaxID=3702;
2 ARYMLLLLLAVWVLTGELWPGAEARAAPYGV--RLCGREFIRAVIFTCGGSRWRRSDILA 59
                                           1151 GIEATRISRGLHLMQRKYI-----TDLLKKHNMLDTKPVSTPMSPTPKLSL 1196
                                                                                                                                                                                     46 -----VGRNNRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| ||:| ||:|| :|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||
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Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
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Best Local Similarity 26.0%; Pred. No. 23;
Matches 39; Conservative 16; Mismatches 39; Indels 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1429 AA; 159492 MW; 7B20CCFB1A9BC263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U1-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) POLYPROTEIN.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
SIMILARITY TO UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1429 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                 120 VLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                          62 INRGIVEECCFRSCDLALLETYC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00665; Tve; 1.
Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; znF_C2HC; 1.
Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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"A set of ordered cosmids and a detailed genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                262 FWGWAEVNIKPWESLLKELREGNERTKW--INREPYAY-----WKGNPMVAETRODLMK 313
                                                                                                                                                                                                                                                                                                                                                                70 ----ADAD---EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLA 122
                                                                                                                                                                                                                                                                                                                                      -----ETLDIVFPDWS 261
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                         20 WP-----GAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPD-- 69
                                                                                                               Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S., Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequent features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetales;
                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                     10.4%; Score 79; DB 10; Length 542; 21.9%; Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  19; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown S.P., Harris D.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan; PF00657; Lipase_GDSL; 1.
SEQUENCE 454 AA; 47507 MW; 9F36FAACF4DBE45D CRC64;
                                                                                                                                                                                                    EMBL; AB005244; BAB10058.1; -. SB3C11327A77F26D CRC64; SEQUENCE 542 AA; 62587 MW; 583C11327A77F26D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL353832; CAB88833.1; ...
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      224 WPVVRATEFAGANAPSPPPLFRYCGNE---------
                                                                                                                                                                                                                                                                                                                                                                                                                          123 GLSSSCCKW-----GCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 :1:::| | 314 CNVSEEHEWNARLYAQDWIKESKEGYKQSDLASQC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                          STRAIN-COLUMBIA;
MEDLINE-97471969; PubMed-9330910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE SECRETED PROTEIN.
                                                                                                                                                                                                                                                                                        34; Conservative
                                                                                                                                                                                           4:215-230(1997).
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                                                                                                                                                                                                                                                              210 VTAVAYTTPTPYWRYLFALDVLSHEADGTVVAFGDSITDGARSQSDANHRWTDVLAARLH 269
                                                                                                                                                                            40 IRAVIFTCGGSRWR---RSDILAHE-----AMGDTFPD-----ADADE---DSLAGELD 82
                                                                                                   37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces pristinaespiralis.
Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97158664; PubMed-9006024; MEDLINE-97158664; PubMed-9006024; De Creey-Lagard V., Blanc V., Gil P., Naudin L., Lorenzon S., Pamechon A., Bamas-Jacques N., Crouzet J., Thibaut D.; Pamechon A., Bamas-Jacques N. Crouzet J., Thibaut D.; Pameshinamycin I biosynthesis in Streptomyces pristinaespiralis: "Pristinamycin I biosynthesis in Streptomyces pristinaespiralis: molecular characterization of the first two structural peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Crecy-Lagard V.A., Saurin W., Thibaut D., Gil P., Naudin L., de Crouzet J., Blanc V.; Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                        83 EAMGS-----SEWLA----LTKSPQAFYRGRPSWQGTPGVLRGSRDVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%; Score 78; DB 2; Length 2591; 27.7%; Pred. No. 75;
10.3%; Score 78.5; DB 2; Length 454; 31.0%; Pred. No. 8.5; tive 12; Mismatches 29; Indels 37
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
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Interpro; IPR003880; Phosphopant_attach.
Pfam; PF00501; AMP-binding; 2.
Pfam; PF00668; Condensation; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50075; ACP_DOMAIN; 2. PROSITE; PS00455; AMP_BINDING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2591 AA; 276024 MW;
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InterPro; IPR000873; AMP-bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X98690; CAA67248.1; -. EMBL; Y11548; CAA72311.1; -.
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                                                                                                                     35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Matches 38; Conserv
                                        Query Match
Best Local Similarity
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Search completed: June 27, 2002, 16:16:28 Job time: 497 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 27, 2002, 16:08:46 ; Search time 18.68 Seconds (without alignments) 294.335 Million cell updates/sec

1 MARYMLLLLLAVWVLTGELW......GLSSSCCKWGCSKSEISSLC 142 US-09-781-077-2 760 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			RELX_SQUAC	INL5_MOUSE	INL5_HUMAN	RELX ODOTA	RELX CANEA	RELX HORSE	REL2 HUMAN	REL2 PANTE	RELX PIG	TNIS BOVIN	TNIS	TNISTATION	PET X MACMIT	RELY DATED	TNI 3 DAM	TNI-3 MOTICE	TNI 3 HIMAN	PELY MOTICE	RELL HIMAN	PELY BAT	PET 1 DANTED	TNT TOPONE	TALE DATE	LIRP LOCMI	INI.6 MOUSE	RELY MECAN	RELH PARTH	TNC DIMAN	TNS DANTE	INS PIG	INS MACEA	INS_ORENI	INL6_HUMAN	
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REIX_BALAC INS_CERAE INS_LOPPI INS_AOTTR INS_AOTTR INS_AOTTR INS_ATRECOLI CATA_RHOCA REIX_BALED INS_CHICK INS_CHICK INS_CHICK INS_CHICK INS_CTDE MPI7_LYMST ALIGNMENTS	JUDARD: PRT; 54 AA. 12, Created) 28, Last sequence update) 29, Last sequence update) 29, Last sequence update) 29, Last sequence update) 20, Last sequence of seq	Score 1 Pred. N 0; Mism RSDILAHE
54 1 110 1 110 1 110 1 110 1 110 1 110 1 100 1 100 1 100 1	LT 1 SGUAC STANDARD; PRT, PRIL, SGUAC PIL193; O1-OCT-1989 (Rel. 12, Created) 16-OCT-2001 (Rel. 28, Last sequency of the state of the	20.1%; larity 28.6%; Conservative 1 EFIRAVIFTCGGSRWR; EFIRAVIYTCGGSR GAFYRGRPSWQGTPGVJ
10.3 10.3 10.1 10.1 10.0 10.0 9.8 9.7 9.7 9.7 9.7	JAC ST. 1989 (Rel. 1994 (Rel. 2001 (Rel. 200	Similarity 12; Conserv LCGREFIRAVI LCGREFIRAVI
78.5 76.58.7 76.58.7 74.76.78.7 73.78.78.7 73.78.78.7 73.78.79.7	**SQUAC***SQUAC***STANDARD; P11953; O1-0CT-1989 (Rel. 12, CI O1-0CT-1989 (Rel. 12, Li o1-01-0CT-1989 (Rel. 12, Li o1-01-0CT-1989 (Rel. 12, Li o1-01-0CT-2001 (Rel. 40, Li o1-0T-1989) (Rel. 28, Li o1-0CT-2001 (Rel. 40, Li o1-0T-1989) (Rel. 20, Rel. 20, Rel	n O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lok S., Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily.";
                                                                                                                                                                                                                                                       Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC DEVELOPMENT AND REGULATION.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                        "cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; wol. Endocrinol. 13:2163-2174(1999).
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INSULIN-LIKE PROTEIN INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSULIN-LIKE PEPTIDĖ INSL5 A CHAIN
                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5):
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
INSL5 OR ZINS3 OR RIF2 OR RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
05FF9A0F613DBF92 CRC64;
                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF054842; AAF09093.1; ALT_INIT.
EMBL; AF054843; AAF09094.1; --
EMBL; BC010968; AAH10968.1; --
                       PRT;
                                                                                                                                                                                                                                                                                                                                                        STEAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                 MEDLINE=99389725; PubMed=10458910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF133817; AAD29687.1; -. EMBL; AF076971; AAD48089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 B
15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1346085; Insl5.
                                                                                                                                                                                                                                                                                                          Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
135 AA;
                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
115
                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue-colon
                           INL5 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
RESULT 2
INL5_MOUSE
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                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENT AND REGULATION.

-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULEIDE BONDS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS IN UPERUS AND ASCENDING AND DESCENDING COLON.

-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                   50 --LEGHFHSQQAETRNYLQLLDRHEPSKKTLEHSLPKTDLSGQELVRDPQAPKEG--LWE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EAMGDIFPDADADEDSLAGELDEAMGSSEWL------ALTKSPQAFYRGRPSWQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Colon;

BEDLINE-99389725; PubMed=10458910;
Conklin D., Lofton Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                         1 MARYMLILLIAWWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN-LIKE PEPTIDE INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INSULIN-LIKE PEPTIDE INSL5 A CHAIN (POTENTIAL).
                                51; Indels 36;
                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE (POTENTIAL).
19.5%; Score 148; DB 1; Length 135; 29.9%; Pred. No. 1.1e-07; tive 21; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98FFCB20E9C4BC1F CRC64;
                                                                                                                                                                                       109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                   PRT;
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Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF133816; AAD29686.1; -.
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135 AA; 15318 MW;
                                                                                                                                                                                                                                                                                                   STANDARD;
                                       46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00078; ILGF;
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
           Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                        INL5_HUMAN
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93 LTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142

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1 QLCGRGFIRAIIFACGGSRWATS--------

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5,
                                                                                                    71 DAD-EDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCC 129
                                                                                                                            86 DASGEDRING-----GOMPIEELWKSKKHSVMSRQD------LOTLCC 122
                                   45; Gaps
                                                                                                                                                                                                                                                                                                                              Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
                                                 32 VRLCGREFIRAVIFTCGGSRWRR-----SDILAH-----EAMGDTFPDA 70
                                                                         26 VRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGNSFQLPHKREFSEENPAQNLPKV 85
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-82004703; PubMed-7274472;
Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.;
"On the primary and tertiary structure of relaxin from the sand tiger
shark (Odontaspis taurus).";
FEBS Lett. 129:80-82(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bullesbach E.B., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias).";
Eur. J. Blochem, 161:335-341(1986).
-1- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
        DB 1; Length 135;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
6122F6604C660607 CRC64;
                            8; Mismatches 39;
 16.6%; Score 126.5; DB 1
30.8%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                        1-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last Sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A01616; RXRKOT.
InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87054035; PubMed=3780747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4730 MW;
                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                         123 TDGCSMTDLSALC 135
                                                                                                                                                        130 KWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family; Hormone.
         Best Local Similarity
                                                                                                                                                                                                                                                                                                                    Relaxin (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=30501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISION TO 20
                        41;
                                                                                                                                                                                                                                                RELX_ODOTA
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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CHAIN
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DISULFID
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                         Matches
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                                                                                                                                                                                                                                                                                                       Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J., Steger K., Steinetz B.G., Fischer B., Canine preprorelaxin: nucleic acid sequence and localization within
                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart D.R., Henzel W.J., Vandlen R.;
"Purification and sequence determination of canine relaxin.";
J. Protein Chem. 11:247-253(1992).
I- FONGTION: Relaxin is an ovarian hormone that acts with estrogen to produce dilatation of the birth canal in many mammals.
I- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Gaps
                                                                                                                                                                                Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELAXIN B CHAIN.
CONNECTING PEPTIDE (BY SIMILARITY).
RELAXIN A CHAIN.
DB 1; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I -> S (IN REF. 2).
220BB0EC99DD302A CRC64;
                                                                                        OFTRM8; 09TRM9; 09N0Z7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.8%; Score 112.5; DB 1
21.5%; Pred. No. 0.00041;
tive 16; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN
                                                                                                                                                                                                                                                                           TISSUR=Placenta;
MEDLINE=99150177; PubMed=10026098;
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta;
MEDLINE=93000391; PubMed=1388669;
                                                                                                                                                                                                                                                                                                                                                                     Biol. Reprod. 60:551-557(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SMUUUTB; ILGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 26-60 AND 154-177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF233687; AAF60302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20563 MW;
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
                                                                                                                                                          Prorelaxin precursor.
                                                                                                                                                                                                                                                                                                                                                           placenta.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                RELX_CANFA
                                                                                                                                                                                                                                                                                                                                                      the canine
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                                                              RELX_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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:99

Score 117; DB 1; Length 44; Pred. No. 3.3e-05; 6; Mismatches 11; Indels

15.4%;

24.5%;

Similarity

Local S. 27;

Matches

Query Match

Conservative

33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWLA 92

THE BUILDING

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.;
"Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.":
                                                                                                                                                      98 RIATRSGKEKLLRELHFVLEDSNLNLEEMKKTFLNTQFEAEDKSLSKLDKHPRKKRDNYI 157
                                                                                                                          -----RGSRDVLA 122
                                                             61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKSPQAFYRGRPSWQGTPGVL 114
                                                                                          55 ------AGQLRERRQISEPLAEVVPSSIINDPEILSIMLQSIPGMPQEL 97
1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                               1 MIRWFLSHLLGVWLLLSQL-PREIPATDDKKLKACGRDYVRLQIEVCGSIWWGRK---- 54
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-HOKKAIDO; TISSUE-Placenta;
Min R., Shiota K., Ogawa T.;
"Molecular cloning of equine preprorelaxin cDNA.";
J. Reprod. Dev. 42:171-178(1996).
                                                                                                                                                                                                                                                                                                       RELX_HORSE STANDARD; PRT; 182 AA. P22969; 028907; 01-8046-1991 (Rel. 19, Created) 01-N0V-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                  PRT; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=91275796; PubMed=2055195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=95359320; PubMed=7543295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Reprod. 52:1307-1315(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB000201; BAA19069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-53 AND 163-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S78800; AAB35036.1; -. PIR; A49739; A49739. PIR; B49739; B49739.
                                                                                                                                                                                            123 GLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                              SEQUENCE OF 32-174 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Prorelaxin precursor (RXN).
                                                                                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placenta.
                                                                                                                                                                                                                                                                                             RELX_HORSE
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SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
MEDLINE-85051298; PubMed-6548702;
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones.";
EMBO J. 3:2333-2339(1984).
                                                                                                                                                                                                                                                                                                                                                             61 EAMGDTFPDADADE-----DSLAGELDEAMGSSEWL--ALTKSPQAFYRGR-PSW---- 107
                                                                                                                                                                                                                                                                                                                                                                                          61 E-----PGLEAGOPVEIVSSSISKDAEALNTKLGLNSNLPKEOKATLSEROPSWRELLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                      115 QPALKDSNLNLEEFEETILKTQSEVEDDSLSELKNLGLDKHSRKKRMIQLSHKCCYWGCT 174
                                                                                                                                                                                                                                                                                                     1 MARYMLILLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                                                                                                                 1 MRRLFLSHVLGAWLLLSQLPRELSGQKPDDVIKACGRELARLRIEICGSLSWKKTVLRLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gunnersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel
alternatively-spliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                            14.5%; Score 110; DB 1; Length 182; 21.8%; Pred. No. 0.00074; tive 25; Mismatches 70; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                             BY SIMILARITY.
A -> V (IN REF. 2).
L -> Q (IN REF. 2).
; E5C9414303A838B8 CRC64;
                                                                                                   CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 185 AA. STANDARD, PRT; 185 AA. P04090; Q9UCX3; Q99936; O1-NOV-1986 (Rel. 03, Last sequence update) O1-NOV-1986 (Rel. 03, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                    RELAXIN A CHAIN.
                                                                                     RELAXIN B CHAIN
InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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              Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN: 1.
Insulin family; Hormone; Signal.
                                                                                                                                                                                             133 L
20721 MW;
                                                                                                                                                                                                                                                                                  41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prorelaxin H2 precursor.
                                                                                                        156
182
169
182
173
66
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                         26
54
161
161
35
17
168
168
133
182 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 RKELAROC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sehra H.;
                                                                                                                                       DISULFID
                                                                                                                                                       DISULFID
                                                                                                                                                                   DISULFID
                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                              SEQUENCE
                                                                              SIGNAL
                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REL2_HUMAN
                                                                                                CHAIN
                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                         -1-SUBCELLULAR LOCATION: Secreted.
-1-ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-1-TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also expressed in placenta, decidua and prostate.
-1-SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                              Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T., Goldsmith L.T.;
                                                                                                                                                      Human seminal relaxin is a product of the same gene as human luteal
                        Buellesbach E.E., Schwabe C., "Total synthests of human relaxin derivatives by solid-phase peptide synthesis and site-directed chain combination." J. Blol. Chem. 266:10754-10761(1991).
                                                                                                                                                                                                                    MEDLINE-91167739, PubMed-2076464; Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.; "Structural characterization by mass spectrometry of native and recombinant human relaxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00262; INSULN; 1.
Insulin family; Hormone; Multigene family; Signal; 3D-structure;
Alternative splicing.
SIGNAL
SIGNAL
25 53 RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                        Biomed. Environ. Mass Spectrom. 19:655-664(1990).
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CONNECTING PEPTIDE.
RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN
            MEDLINE=91250367; PubMed=2040595;
                                                                                                                                                                                Endocrinology 130:2660-2668(1992).
                                                                                                                  MEDLINE=92241162; PubMed=1572287;
                                                                                                                                                                                                       SEQUENCE OF 25-53 AND 162-185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00948; CAA25460.1; --
EMBL; AL135786; CAC04177.1; --
EMBL; AL135786; CAC04176.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S83200; AAD14429.1;
EMBL; A17315; CAA01324.1;
EMBL; A06925; CAA00602.1;
PIR; A60982; A60982.
                                                                                      PARTIAL SEQUENCE OF 25-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00078; ILGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6RLX; 31-0CT-93.
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                                                                                                                                                                      relaxin.
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DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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EIVPSFINKDTETINMMSEFVANLPQELKLTLSEMQPALPQ
                       LOQHVP -> GDFIGTVSLGISPDGGRALRTGSCFTREFLG
ALSKLCHPSSTKIQKP (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAPQTPRPVAEIVPSFINKDTETINMMSEFVANLPQELKLTLSEWQPALPQLQQHVPVLK 120
                                                                                                                                                                                                                                                                                                               121 DSSLLFEEFKKLIRNRGSEAADSSPSELKYLGLDTHSRKKRQLYSALANKCCHVGCTKRS 180
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                       1 MARYMLLLLLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAH 60
                                                                                                                                                                                                                                     61 EAMGDIFPDADADEDSLAGELDEAMGSSEWLA-----LTKS-----PQ----- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                            43;
                                                                                                                                                                             14.4%; Score 109.5; DB 1; Length 185; 22.7%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans B.A., Fu P., Tregear G.W.; "Characterization of two relaxin genes in the chimpanzee.";
                                                                                                                                            21042 MW; AC73DBDE2090091B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILT. PANTR STANDARD; PRT; 166 AA. P51455; P79267; STANDARD; PRT; 166 AA. P51455; P79267; STANDARD; PRT; 166 AA. D1-CCT-1996 (Rel. 34, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                       22.7%; Preα. ...
Five 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prorelaxin H2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
MEDLINE=94238260; PubMed=8182365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinol. 140:385-392(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                      Conservative
                                                                                                                                            185 AA;
                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                          138 ISSLC 142
                                                                                                                                                                                                                                                                                                                                                                               181 LARFC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNL2 OR RLX2
                                                                                                                                                                                                    42;
  DISULFID
           VARSPLIC
                                          VARSPLIC
                                                                                                                                            SEQUENCE
                                                                                                                                                                             Query Match
                                                                 STRAND
                                                                                                            STRAND
                                                      HELIX
                                                                                     HELIX
                                                                                                                       HELIX
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SECUENCE OF 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB;
PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                       EIVPSFINKDTETINMMSEFVANLPQELKLTLS -> DFIQ
                                                                                                                                                                                                                                                                                                                                                                                                                      TVSLGISPDGGKALRTGSCFTREFLGALS (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 A-----LTKS-----WQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 ANLPQELKLILSEMQPALPQLQQYVPVLKDSSLLFEEFKKLIRNRQSEAADSSPSELKYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 VRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 IKLCGRELVRAQIALCGKSTWSKRSLSQEDAPQTPRPVAEIVPSFINKDTETINMMSEFV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87308187; PubMed-2442155;
Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.
produced by alternative splicing.
TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
AND IN THE PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                     SMART; SMO0078; IlGF: 1.
PROSITE; PS00262; INSULIN: 1.
Insulin family; Hormone; Multigene family; Signal; Polymorphism;
Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 108.5; DB 1; Length 166; 23.4%; Pred. No. 0.00094; tive 20; Mismatches 55; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSTWS -> MSTLG (IN SOME ALLELES).
220851E3134CEBDB CRC64;
                                                                                                                                                                                                                                                                                                                   POTENTIAL.

RELAXIN B CHAIN (PROBABLE).

CONNECTING PEPTIDE (PROBABLE).

RELAXIN A CHAIN (PROBABLE).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).
                                         -! - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                     InterPro; IPR000739; Insulin_IGF_relaxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 AA; 18760 MW;
                                                                                                                                                                                EMBL; Z27245; CAA81758.1; -.
                                                                                                                                                                                                 AAD14430.1; -.
                                                                                                                                                                                                                                        Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
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138
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157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Niall H.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-i- SUBDNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schwabe C., McDonald J.K.; "Demonstration of a pyroglutamyl residue at the N terminus of the B-chain of porcine relaxin."; Biochem. Biophys. Res. Commun. 74:1501-1504(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G., Evans A., North A.C.T. "Relaxin and its structural relationship to insulin.";
Nature 271:278-281(1978).
                                                                                                                                                                                                                                                                                                                                                                        James R., Niall H., Kwok S., Bryant-Greenwood G.; "Primary structure of porcine relaxin: homology with insulin and
                                                                                                         SEQUENCE FROM N.A.
MEDLINE-83157118; PubMed-6897721;
Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBGELLULAR LOCATION: Secreted.
                                                                                                                                                                                                        Tregear G., Niall H.; "Porcine relaxin: molecular cloning and cDNA structure."; DNA 1:155-162(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-76231539; PubMed-938497; Schwabe C., McDonald J.K., Steinetz B.G.; Primary structure of the A chain of porcine relaxin."; Primary structure of the A chain of porcine relaxin."; Plochem. Blophys. Res. Commun. 70:397-405(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwabe C., McDonald J.K., Steinetz B.G.; "Primary structure of the B-chain of porcine relaxin."; Biochem. Biophys. Res. Commun. 75:503-510(1977).
"Porcine relaxin. Gene structure and expression.";
J. Biol. Chem. 262:11940-11946(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schwabe C., McDonald J.K.; "Relaxin: a disulfide homolog of insulin."; Science 197:914-915(1977).
                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 25-54 AND 161-182.
MEDLINE-77213067; Pubmed-876374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE MODELING.
MEDLINE=78092399; PubMed=622170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=77236040; PubMed=887933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=77134136; PubMed=843375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; KO1088; AAA31114.1; --
EMBL; J02792; AAA31115.1; --
EMBL; A16593; CAA01295.1; --
EMBL; A06652; CAA00600.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                         related growth factors.";
Nature 267:544-546(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2RLX; 15-OCT-94.
3RLX; 15-OCT-94.
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A29796; A29796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 161-182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 25-51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                    69 DADA------DEDSLAGELDEAMGSSEWLALTKSPQAFYRGRPSWQ------- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GTPGVLRGSRDVLAGLSSSCCKWGCSKSEISSLC 142
                                                                                                                                                                                                                                                                                                    14.0%; Score 106.5; DB 1; Length 182;
21.7%; Pred. No. 0.0016;
tive 22; Mismatches 68; Indels . 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FEEFKKIILNRQNBABEDKSLLELKNLGLDKHSRKKRLFRMTLSEKCQVGCIRKDIARLC 182
                                                                                                                                                                                                                                                                                                                                                          9 LLAVWVLTGELWPGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFP 68
                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Testis;
MEDLINE=97107158; PubMed=8949906;
Bathgate R.A.D., Balvers M., Hunt N., Ivell R.;
"Relaxin-like factor gene is highly expressed in the bovine ovary of the cycle and pregnancy: sequence and messenger ribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNTY: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Reprod. 55:1452-1457(1996).
-1- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                             WGRT -> TWGR (IN REF. 3).
S -> L (IN REF. 1).
Q -> E (IN REF. 6).
20736BB089F13AB4 CRC64;
                                                                                                                                                                                                  G -> GVWS (IN REF. 4).
                                                                                                             CONNECTING PEPTIDE. RELAXIN A CHAIN.
                                                                 Hormone; Signal; 3D-structure.
                                                                                               RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 AA.
InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                        INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
              Pfam; PF00049; Insulin; 1.
SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                            20818 MW;
                                                                                                                                                                                                                                                                                                                                 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                          154
182
25
169
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                          Insulin family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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DISULFID
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INL3_BOVIN
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                              80 E--LDEAMGSSE---WLALTKSPQA--FYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWG 132
                                                                                                                                                                                                                                                                                                                                                                                                                            74 QHLLHGLWASGDPVLVLAPQPLPQASRHHHHRRATAINP-----ARHCCLSG 120
                                                                                                                                                                                                                                                                                                            43; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                   23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDS---LAG 79
                                                                                                                                                                                                                                                                                                                                                    Adham I.M., Burkhardt E., Benahmed M., Engel W.;
"Cloning of a CDNA for a novel insulin-like peptide of the testicular
Leydig cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural organization of the porcine and human genes coding for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leydig cell-specific insulin-like peptide (LEY I-L) and chromosomal localization of the human gene (INSL3) ", Genomics 20:13-19(1994).
                                                                                                                                    LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTEWTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
                                                                                                                                                                                                                                                                            13.6%; Score 103.5; DB 1; Length 132; 28.5%; Pred. No. 0.0023; Live 17; Mismatches 43; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTNATAL LEYDIG CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                   BY SIMILARITY.
A5585500C7F2241D CRC64;
                                        InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMARI; SM0078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
or send an email to license@isb-sib.ch).
                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 268:26668-26672(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;
MEDLINE=94075362; PubMed=8253799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=94292172; PubMed=8020942;
                                                                                                                                                                                                                              132 AA; 14378 MW;
                           EMBL; AF094580; AAC63380.1;
                                                                                                                                                                                                                                                                    Query Match 13.6%
Best Local Similarity 28.5%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                      57
104
132
117
117
130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CTRODLLTLC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
"Differential splicing and expression of the relaxin-like factor gene in reproductive tissues of the marmoset monkey (Callithrix jacchus)."; Biol. Reprod. 60:445-453(1999).
-!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INL3_CALJA STANDARD; PRT; 131 AA.
097937; 097938;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULETDE BONDS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORY/TRUNCAFED FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN THE LEYDIG CELLS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 ELL---OWLEGQHLFHGLMASGDPMLVLAPOPPPQAS-GHHHHRRAAATNPARHCCLSGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 EAMGSSEW-----LALIKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 APAQEAP--EKLCGHHFVRALVRLCGGPRW------SPEDGRAVAGGDR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                    C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
                                                                                                                                                                                                                                                                                                 LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 102; DB 1; Length 131; 24.8%; Pred. No. 0.0031; tive 19; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (BY SIMILARITY). INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                             8AB718870859EF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=99115234; Pubmed=9916013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                       Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            callithrix jacchus (Common marmoset)
Eukaryota, Metazoa; Chordata, Crania
                                                                                                                                                                                                                                                                    Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                   14134 MW;
                                                                                                                                                            EMBL; X73636; CAA52016.1; -. EMBL; X68369; CAA48449.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Conservative
                                                                                                                                                                                                                                                                                                       56
103
131
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129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9483;
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9
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J. Mol. Endocrinol. 3:169-174(1989).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO
-!- FUNCTION: RELAXINI IS AN OVARIAN HORMONE THAT MANMALS. MAY BE
PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE
INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNANCY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90073957; PubMed=2590381;
Crawford R.J., Hammond V.E., Roche P.J., Johnston P.D., Tregear G.W.;
Structure of rhesus monkey relaxin predicted by analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 RRHLLYGLVANSEPA--PGGPGLQPMPQTSHHHRHRRAAASNPARYCCLSGCSQQDLLTL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 -----ALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSS---CCKWGCSKSEISSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 RLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEAMGSSEWL- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 KLCGHHFVRALVRVCGGPLW-STEARRPVAAGD------GEL-----LOWLE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      GELLQWLERRH -> ESHSAAQDGGQ (IN SHORT
                                                                                                                                                                                                                                                                                                                      LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                          C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 131;
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSING (IN SHORT ISOFORM).
685743CAEECF8731 CRC64;
                                                                                                                                                                                                                                                                                            Hormone; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 101.5; DB 1
28.1%; Pred. No. 0.0035;
tive 13; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA.
                                                                                                                                                                                                                                Interpro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                               EMBL, AJ011961; CAA09888.1; -.
EMBL, AJ011962; CAA09888.1; JOINED.
EMBL, AJ011961; CAA09889.1; -.
HSSP; P01315; 1ZEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14252 MW;
                                                                                                                                                                                                                                            Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 28.18
hes 34; Conservative
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130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 AA;
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58
107
34
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116
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                                                                                                                                                                                                                                                                                                     Insulin family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EAMGDTFPDADADEDSLAGELDEAMGSSEWLA-----LTKSP-----97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raja erinacea (Little skate).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Chondrichthyes;
PROMOTING GROWTH OF PUBIC LICAMENTS AND RIPENING OF THE CERVIX. SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87156758; PubMed-3827922;
Bullesbach E.E., Schwabe C., Callard I.P.;
Bullesbach from an oviparous species, the skate (Raja erinacea).";
Biochem. Biophys. Res. Commun. 143:273-280(1987).
-:- SUBUNT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elasmobranchii, Squalea, Hypnosqualea; Pristiorajea, Batoidea, Rajiformes, Rajidae, Raja.
NCBL_TaxID=7782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 101.5; DB 1; Length 185; Similarity 22.7%; Pred. No. 0.0051; L2; Conservative 22; Mismatches 78; Indels 43
                                                                                                                                                                                                                                                                           RELAXIN B CHAIN (PROBABLE).
CONNECTING PEPTIDE (PROBABLE).
RELAXIN A CHAIN (PROBABLE).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                          -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                           7E3C5D21B57E185C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 AA
                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                            InterPro; IPR000739; Insulin_IGF_relaxin.
Pram; PR00049; Insulin; 1.
SWART; SW00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000739; Insulin_IGF_relaxin_Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                        Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                        20895 MW;
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                                                                                                      PIR; A34936; A34936.
HSSP; P04090; 6RLX.
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HSSP; P04090; 6RLX.
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56
161
151
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171
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185 AA;
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P11952:
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Best Local S
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                                                                                                                                                                                                                                                                         CHAIN
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RELX_RAPER
ID RELX_RAPER
DT 01-0CT
DT 16-0CT
DT 16-0CT
DE Relaxi
OS Raja e
OC Elasmo
OC Elasmo
OC Rajifo
OX NOBL_T
RN [1]
RN [1]
RN [1]
RN [1]
RN SEDUEN
RC TISSUE
RX MEDLIN
RC Balles
RX MEDLIN
RC Balles
RX MEDLIN
RC IISSUE
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RC BIOCH
CC -: SU
CC -: SU
CC -: SI
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                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                              81 LDEAMGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVLAGLSSSCCKWGCSKSEISS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                21 PGAEARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGE 80
                                                                                                                                                                                                                                                   40 MEEKM------GFAKKCCAIGCSTEDFRM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                              / Match 13.2%; Score 100.5; DB 1; Length 64; Local Similarity 22.1%; Pred. No. 0.002; nes 27; Conservative 11; Mismatches 25; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spiess A.-N., Pusch W., Ivell R.;
"Cloning and sequence of the rat relaxin-like factor and its
promotor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
LeCOT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
                                                                                                                E7AC62B8BA81F49D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C PEPTIDE (POTENTIAL).
                 RELAXIN B CHAIN.
                                                RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                 INTERCHAIN.
                                                                                  INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF139918; AAD33663.1; -.
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41
64
51
64
55
7499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
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NON_TER 1
CHAIN <1
PROPEP 7
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                                                                                                                                                                                                                                                                                                                                                                                               63 VC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment)
                               NON_CONS
CHAIN
                                                                            DISULFID
                                                                                                              SEQUENCE
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                                                               DISULFID
                                                                                                                                                                Query Match
                                                                                                                                                                                              Matches
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FT FT FT
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	6 ;				
105 LEYDIG INSULIN-LIKE PEPTIDE A CHAIN. 90 INTERCHAIN (BY SIMILARITY). 103 INTERCHAIN (BY SIMILARITY). 94 BY SIMILARITY. 11674 MW; 903716ABFBB13EE CRC64;	Query Match Best Local Similarity 24.8%; Pred. No. 0.0035; Matches 35; Conservative 11; Mismatches 34; Indels 61; Gaps	25 ARAAPYGVRLCGREFIRAVIFTCGGSRWRRSDILAHEAMGDTFPDADADEDSLAGELDEA 84	85 MGSSEWLALTKSPQAFYRGRPSWQGTPGVLRGSRDVL 121 11 1 1 1 39 LQWLEQRHLLHALVADADADPALDPQLPHQASQRQRRSVA 82	122 AGLSSSCCKWGCSKSEISSLC 142 :::: 83 TNAVHRCCLTGCTQQDLLGLC 103	Search completed: June 27, 2002, 16:16:51 Job time: 485 sec
80 6 18 89 105 AA;	Similarity 5; Conser	APYGVRLCGRI : KLCGHI	85 MGSSEWL : 39LQWLEQRHLL	SSSCCKWGCSI 	ted: June Sec
CHAIN DISULFID DISULFID DISULFID SEQUENCE	ery Match st Local tches 3	25 ARA ARA	85 MGS	122 AGL 83 TNA	Search completed: Job time: 485 sec
FF	Ou Be Ma	Oy Db	Qy Dp	Qy	Sear

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

June 27, 2002, 16:08:09; Search time 73.16 Seconds (Without alignments) 36.438 Million cell updates/sec

US-09-781-077-2_COPY_119_142

1 DVLAGLSSSCCKWGCSKSEISSLC 24 Perfect score: Sequence:

Scoring table:

747574 seqs, 111073796 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

Database :

| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1983.DAT:
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1984.DAT:
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:
| SIDS1/gcddata/hold-geneseq/geneseqp-embl/Aa1986.DAT:
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| SIDS1/gcddata/hold-geneseq/geneseqfyeneseqp-embl/Aa1989.DAT:
| SIDS1/gcddata/hold-geneseq/geneseqfyeneseq /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS1/geneseqp-embl/AA1999.DAT:*/SIDS1/geneseqp-embl/AA1999.DAT:*/SIDS1/geneseqp-embl/AA1999.DAT:*/SIDS1/geneseqp-embl/AA1999.DAT:* /SIDS1/gogdata/hold-geneseg/genesegp-embl/AA1998.DAT:*/SIDS1/gogdata/hold-geneseg/genesegp-embl/AA1999.DAT:*/SIDS1/gogdata/hold-geneseg/genesegp-embl/AA2000.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981. A_Geneseq_032802:* 14: 15: 16: 17: 18: 19: 20: 22:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Human insulin homo Mouse Zinsi proteil Mouse insulin fami Human zinsi testis Rat Zinsi testis Sequence encoded b Sequence of porcin Sequence of porcin Insulin-like pepti Human Zinsi proteil
SUMMARIES	h DB ID	2 22 AAG78114 5 19 AAW37926 5 12 AAV95771 3 19 AAW47548 8 19 AAW47547 2 4 AAP30192 2 4 AAP30192 2 5 AAP401965 5 19 AAW37925
de (Query Match Length DB	1000.0 142 47.7 135 46.2 213 46.2 213 44.7 188 43.9 182 43.9 182 43.2 27 43.2 135
	Score	132 63 63 61 61 61 58 58 58 57 57
1 1 1 1 1	NO.	1 2 2 4 4 4 7 7 7 10 11 11

E (1)	E (1) (1)	Muusu BSK Peceptor Human relaxin A-ch Human immune/haema Prorelaxin A-chain Relaxin analogue A Locust Lirp insuli Prolelaxin fragme H2 prorelaxin fragme	seg seg di di ter th	Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia
AAY01961 AAB00173 AAB24391 AAY95770 AAX8328			∢	AAG14879 AAG49241 AAG49246 AAG08133 AAG14878 AAG49240 AAG49245
221122	22 22 17 20 21 21	16 16 18 18 21 11	11 22 22 23 21 23 21	21 21 21 21 21 21 21 21 21 21 21 21 21 2
135 135 135 135	135 135 928 1005 91	162 162 150 150	164 185 185 133 868 93	313 325 325 325 325
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4			8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
57 57 57 57 57	57 57 57 58 55	83 80 80 80 80 80 80 80 80 80 80 80 80 80	52 51.5 51.5 51.5	51 51 51 51
12 13 14 15 17 17	20 20 22 23 24	25 22 33 33 31) 4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

antifertility; vasotropic; reproductive disorder; prostate disorder; heart disorder; kidney disorder; gonadal development; pregnancy; pubbertal change; menopause; ovarian cancer; testicular cancer; coulation; polycystic ovarian syndrome; contractile tissue; cardiovascular disease; birth control; impotence; myocyte; endothalial cell; osteoblast; blood pressure; muscle tension; osmotic balance; gene therapy. Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; /label= B_chain_consensus_sequence_region /note= "Given in SEQ ID NO 3" 37..41 /label- signal_peptide 26..142 /label- mature_protein /note= "Zins4, claimed in claim 4" 'note= "Claimed in claim 1" Human insulin homologue polypeptide Zins4. AAG78114 standard; Protein; 142 AA. Location/Qualifiers /label- B_chain (first entry) Homo sapiens. 21-NOV-2001 AAG78114; Peptide Protein Region Region Region AAG78114 RESULT

/label= B_chain_conserved_motif

~

1 DVLAGLSSSCCKWGCSKSEISSLC 24

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/note= "Cleavage site at the junction of the C peptide and the A chain with a conserved RXXR motif"
                                                                         /label= A_chain_consensus_sequence_region
/note= "Given in SEQ ID NO 4"
"Given in SEQ ID NO 5"
                                                         /label= A_chain
/note= "Claimed in claim 2"
                            "Claimed in claim 3"
                                                                                                                                                   Holloway JL, Lok S, Jaspers SR;
                 /label = C_peptide
                                                                                                                            10-MAR-2000; 2000US-0523346.
                                                                                                                 09-FEB-2001; 2001WO-US04199.
                                                                                                                                        (ZYMO ) ZYMOGENETICS INC.
                                                                    .142
                                  118
                                                   119..142
            .118
 /note=
53..54
                            /note=
                                                                                                                                                              WPI; 2001-582454/65.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 142 AA;
                                                                                                                                                                    N-PSDB; AAH79088.
                                                                                            WO200168862-A1
                                   Cleavage-site
        Cleavage-site
                                                                                                       20-SEP-2001
                                                    Region
                                                                      Region
                         Region
              Region
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The invention relates to an isolated insulin homologue zins4 having

C fomology to the relaxin family. The zins4 gene, located on chromosome

CC 1913.11, encodes a 142 amino acid protein, where the Zins4 polypeptide

CC comprises a B chain and A chain comprising amino acid residues 26-52 and

CC comprises a B chain and A chain comprising amino acid residues 26-52 and

CC zins4 has cytostatic, antifertility and vasortopic activity. Zins4

CC zins4 has cytostatic, antifertility and vasortopic activity. Zins4

CC zins4 has cytostatic, antifertility and vasortopic activity. Zins4

CC zins4 has cytostatic, antifertility and vasortopic activity. Zins4

CC zins4 has cytostatic zins4 protein is useful in treating reproductive,

CC reproductive disorders. Zins4 protein is useful in treating of eproductive,

CC cell lines which respond to the zins4-stimulated pathway and to identify

CC inhibitors of its activity. Zins4 polypeptides and modulators of the

CC plypeptide are useful in treating disorders associated with gonadal

CC development, pregnancy, pubertal changes, menopause, ovarian cancer,

CD prostate, testicular cancer, fertility, ovarian function, ovulation,

CC prostate, testicular cancer, fertility, ovarian function, ovulation,

CC prostate, testicular cancer, fertility, ovarian function associated

CC prostate, testicular and patient is useful for diagnosing ovarian

CC prostate, testicular and patient is useful for diagnosing ovarian

CC serum or tissue blopsy of a patient is useful for treating disorders are also useful for treating disorders are contractility in vivo,

CC cancer. The molecules are also useful for treating disposing ovarian in the contractile tissues or to suppress or enhance contractility in vivo,

CC treating candiovascular disease, infertility, in vitro fertilization,

CC treating candiovascular disease, infertility, in vitro fertilization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             birth control, treating importence or other male reproductive dysfunction, inducting birth, for promoting growth, differentiation, development and/or maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in culture and in the study of the ovarian cycle, reproductive function, ovarian cell-cell interactions and fertilisation. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic balance. The zins4 polynucleotide is useful in gene therapy.
New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 72-73; 79pp; English.
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Gaps

ö

o 100.0%; Score 132; DB 22; Length 142; Similarity 100.0%; Pred. No. 1.5e-09; 24; Conservative 0; Mismatches 0; Indels 0;

24;

Query Match Best Local S Matches

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associated with the polypeptide, such as reproductive disorders associated with the placente and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Zins3 protein is an insulin homologue protein. Polynucleotide molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a nonhuman animal. The polypeptides can be used to identify and isolate nonhuman animal. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insulin homologue polypeptide(s) and antagonists – used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                    Insulin homologue; identification; isolation; Zins3 receptor; treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 63; DB 19; Length 135; 52.6%; Pred. No. 0.88; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conklin DC, Jaspers SR, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   49..115
/note= "C-peptide"
116..135
                                                                                          AAW37926 standard; Protein; 135 AA.
/note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 67; 81pp; English.
                                                                                                                                                                                                                                                                                                                                    /note= "B chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0028177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US18593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.69
Matches 10; Conservative
                                                                                                                                                            01-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-251285/22.
                                                                                                                                                                                            Mouse Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV29153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-0CT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9816635-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1998.
                                                                                                                               AAW37926;
                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                             Mus sp.
                                                                  RESULT
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173 gysekccltgctkeelsiac 192
                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davis S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAW47548
                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a murine paralog (see AAY95771) of funnan zins3 (see AAY95770), a novel member of the insulin/relaxin family member that maps to a region of human chromosome 1 associated with non-insulin dependent diabetes mellitus (NIDDM). The sequence blots of embryo tissue indicated that mouse zins3 is expressed in a developmentally regulated fashion. Zins3 polynucleotides and a developmentally regulated fashion. Zins3 polynucleotides and abnormal expression of zins3, and to identify polynorphisms that result from mutations in the human zins3 gene. The invention provides methods for identifying abnormalities in expression that are a factor in causing, or predisposing, a person to some defect in glucose metabolism, such as NIDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE, Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.7%; Score 63; DB 21; Length 135; 52.6%; Pred. No. 0.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                        Zins3; insulin; relaxin; mouse; NIDDM;
non-insulin dependent diabetes mellitus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                  Mouse insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 46-47; 51pp; English.
                                                                                                     AAY95771 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW17675 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
117 lqalccregcsmkelstlc 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0198248.
99US-0250125.
                                                                                                                                                                                              (first entry)
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| 117 | Iqalccregcsmkelstlc | 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 52.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA50153
                                                                                                                                                                                                                                                                                                                                                                             WO200047776-A2.
                                                                                                                                                                                     07-NOV-2000
                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-1999;
12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2000.
                                                                                                                                                 AAY95771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW17675;
                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW17675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                             A X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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New isolated relaxin-related factor genes - used to develop products which can be used in diagnosis and therapy, e.g. in fertility and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                             Relaxin-related factor-1; RRF-1; testis; sperm; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .<u>`</u>
                                                                                                                                                                                                                                                                   /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                        /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "conserved Cys residue indicative of insulin family member"
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "conserved Cys residue indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.2%; Score 61; DB 18; Length 213;
50.0%; Pred. No. 2.4;
tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                  insulin family member"
                                                                                                                                                                                                                                                                                                                                                                    insulin family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin family member"
Human relaxin-related factor-1 (RRF-1).
                                                                                                                                                                                                                label Sig_peptide
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US17342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GLSSSCCKWGCSKSEISSLC 24
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Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 192
/note=
                                                                                                                                                                                                                                                                                                            Misc-difference 179
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-272118/24.
                                                                                                                                                                                                                                       Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT68418.
                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9716549-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996;
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                                                                       infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-1996;
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Stewart AG,
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       Rattus rattus
                                                                                         21-NOV-1996;
                           WO9805782-A1.
                                                                                                   02-AUG-1996;
                                                                    01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP68375-A.
                                               12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP30192;
                                                                                                                                                                                                                                                                                                                                                                      Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                       Testis-specific insulin homologue poly:peptide(s) - may be used, e.g. in enhancing viability of cryo:preserved sperm, enhancing sperm motility or in immuno:contraception methods
                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human zins2 testis-specific insulin homologue, which may be used to enhance the viability of cryopreserved sperm, sperm motility, egg/sperm interactions, fertilisation or proliferation or differentiation of testicular cells. Zins2 may also be used as a vaccine, e.g. in immunocontraception methods to prevent fertilisation. Antagonists, e.g. anti-zins2 binding protein, may be used in contraception. Zins2 is especially useful for in vitro fertilisation methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; Zins2; testis-specific insulin homologue; differentiation; cryopreserved sperm viability; sperm motility; proliferation; egg/sperm interaction; fertilisation; testicular cell; vaccine; immunocontraception; contraception; in vitro fertilisation.
                                                                                                                                                                                                                                                                            Adams RL, Conklin DC, Jaspers SR, Jelmberg AC, Lofton-Day CE;
                                                                                  Human; Zins2; testis-specific insulin homologue; differentiation; cryopreserved sperm viability; sperm motility; proliferation; egy/sperm interaction; fertilisation; testicular cell; vaccine; immunocontraception; contraception; in vitro fertilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%; Score 61; DB 19; Length 213; 50.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Zins2 testis-specific insulin homologue.
                                                                  Human Zins2 testis-specific insulin homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.4;
;; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Pages 73-74; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47547 standard; Protein; 188 AA.
      AAW47548 standard; Protein; 213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 gysekccltgctkeelsiac 192
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                                                                                                                                                                                                                                         96US-0023213.
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                                                                                                                                                                                                            97WO-US13879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.03
Matches 10; Conservative
                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                  WPI; 1998-145618/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA;
                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV18663.
                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                    W09805782-A1
                                                                                                                                                                                                                                  21-NOV-1996;
                                                                                                                                                                                                                                            02-AUG-1996;
                                                   03-JUL-1998
                                                                                                                                                                                         12-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                               AAW47548;
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AAW47547
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Gaps
                                                                                                                                                                                                                                                                                                         Testis-specific insulin homologue poly:peptide(s) - may be used, e.g. in enhancing vlability of cryo:preserved sperm, enhancing sperm motility or in immuno:contraception methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is rat Zins2 testis-specific insulin man be used to enhance the viability of cryopreserved sperm, sperm motility, egg/sperm interactions, fertilisation or proliferation or differentiation of testicular cells. Zins2 may also be used as a vaccine, e.g. in immunocontraception methods to prevent fertilisation. Antagonists, e.g. anti-Zins2 binding protein, may be used in contraception. Zins2 is especially useful for in vitro fertilisation methods.
                                                                                                                                                            Adams RL, Conklin DC, Jaspers SR, Jelmberg AC, Lofton-Day CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoded by synthetic gene for porcine relaxin A chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.7%; Score 59; DB 19; Length 188;
45.0%; Pred. No. 3.8;
tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Pages 66-67; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP30192 standard; Protein; 22 AA.
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163 gfadkccaigcskeelavac 182
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97WO-US13879.
                                                                       96US-0023213.
                                                  96US-0031592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                       WPI; 1998-145618/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AA;
                                                                                                                                                                                                                                                                                 N-PSDB; AAV18662.
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WPI; 1983-04897K/03.

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Sequence 182 AA;
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                                                                                                                                                                                                    Gaps
                                                                                  The genes
                                                                         The inventors claim synthetic genes for porcine relaxin. The genes may contain, in addn to the coding sequence, a stop codon, an initiator methionine codon, restriction sites for Cla I and Bam HI etc. Porcine relaxin is useful in the induction and control of labour in women. In sows admin. during farrowing may reduce the rate of still birth of piglets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genes and DNA transfer vectors for prorelaxin expression - useful in prodn. of porcine relaxin for veterinary and human use
                                                                                                                                                                                                    ;
0
                           Prodn. of porcine relaxin from synthetic genes - useful for induction and control of labour in women
                                                                                                                                                                          43.9%; Score 58; DB 4; Length 22; 47.4%; Pred. No. 0.74; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shine J;
                                                                                                                                                                                                                                                                                AAP30392 standard; Protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                          Sequence of porcine preprorelaxin.
                                                        Disclosure; Fig 1; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 5; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Niall HD,
                                                                                                                                                                                                               6 LSSSCCKWGCSKSEISSLC 24
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83AU-0011834.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOWA-) HOWARD FLOREY INST
                                                                                                                                                                                            9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1983-748587/35.
                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                                                                                                                                               22 AA;
           N-PSDB; AAN30124
                                                                                                                                                                                                                                                                                                                                                             Relaxin; hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                  EP86649-A.
                                                                                                                                             Sequence
                                                                                                                                                                          Query Match
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                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The inventors claim the gene for the expression of human preprorelaxin (HPP) and its sub-units. Also claimed are synthetic HPP, HP, fragments and analogues. Human relaxin and its analogues are prepd. for therapeutic purposes, esp. in clinical intervention in cases of difficult labour.
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                      DB 4; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 5; Length 182;
Pred. No. 5;
4; Mismatches 6; Indels
                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hudson PJ, Shine J, Niall HD, Tregear GW;
                                                    4; Mismatches
                                      Pred. No. 5;
                     43.9%; Score 58; 47.4%; Pred. No.
                                                                                                                                                                                               AAP40156 standard; Protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                 Sequence of porcine preprorelaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= C-peptide
161.182
                                                                                                                                                                                                                                                                                                                                 Labour; birth; hormone; relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 3; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26..57
/label- B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161..182
/label= A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= signal
                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83EP-0304662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82AU-0005352.
83AU-0017906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88EP-0104503
Query Match
Best Local Similarity 4/...
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN40125, AAN40126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOWA-) HOWARD FLOREY INST.
                                                                                                                                                                                                                                                                  11-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FLOR-) HOWARD FLOREY INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LSSSCCKWGCSKSEISSLC 24
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP101309-A.
                                                                                                                                                                                                                                AAP40156;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                Pig.
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01-SEP-1998 (first entry)
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                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  15-0CT-1996;
                                                                                                                                                                                                                                                                                                                                   WO9816635-A1
                                                                                                                                                                                                                                                                                                                                                                   23-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
              AAW37925;
                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                    Peptide
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ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents insulin-like polypeptide (pro-ILP)
chain A peptide. The ILP protein is expressed in the colon and uterus,
and is a member of the insulin/IGF family. The immature pro-ILP
comprises a 135 amino acid sequence, which is processed into the mature
form which comprises an A chain and a B chain linked by disulfide bonds.
The Creptide of pro-ILP satists as a separate peptide after processing
of pro-ILP. The ILP protein is useful in treatment of disorders related
to neurophysiological function affecting fluid homeostasis, electrolyte
homeostasis, cardiovascular function, blood pressure, somatic or cardiac
ionotropic activity, cardiac chronitropic activity and collagen
conoctasis, condition of the uterus, colon or other ILP-expressing cell
pathodic condition of the uterus, colon or other ILP-expressing cell
or tissue and for diagnosis and screening of modulators and therapeutics.
In the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                 Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac inotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                        Insulin-like peptide (pro-ILP) chain A peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              created using information provided.
                                                                                                       AAY01962 standard; Peptide; 27 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page -; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.48;
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9 lqtlcctdgcsmtdlsalc 27
        98WO-US17888.
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Matches 9; Conservative
                                                                                                                                                                          01-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-254713/21.
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                                                                                                                                                                                                                                                                                                                                                                               WO9915664-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                              AAY01962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW37925
                                                                                             AAY01962
                                                                           RESULT
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associated with the polypeptide, such as reproductive disorders associated with the placente and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a confuman animal. The polypeptides can be used to identify and isolate receptors for zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and be used for treating also be used in the diagnosis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin homologue polypeptide(s) and antagonists - used to, e.g. treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                           Insulin homologue; identification; isolation; Zins3 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Score 57; DB 19; Length 135;
47.4%; Pred. No. 5.1;
tive 5; Mismatches 5; Indels
                                                                      treatment; disease; pre-elampsia; premature labour; Human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Zins3 protein is an insulin homologue protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lofton-Day CE,
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                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 64-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                 "C-peptide"
                                                                                                                                                                                                                                                            "B chain"
                                                                                                                                                                                                                                                                                                                                                                           /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 lqtlcctdgcsmtdlsalc 135
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                                                                                                                                                                                                                                                                                                                    /note= "C
115..135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                        .114
                                                                                                                                                                                                                                23..48
/note=
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N-PSDB; AAV29150.
Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
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human.

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The present sequence represents an insulin-like polypeptide (pro-ILP). The protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises an A chain and a B chain linked by disulfide bonds. The C-peptide of Pro-ILP exists as a separate peptide after processing of pro-ILP. The neurophysiological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac inonctropic activity, cardiac chrontcopic activity and collagen deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and screening of modulators and therapeutics.
                                           Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                          Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder; angiogenic disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.2%; Score 57; DB 20; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.1;
5; Mismatches
                        Pro-insulin-like peptide (pro-ILP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB00173 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                          Claim 5; Fig 6B; 75pp; English.
                                                                                                                                                                                   98WO-US17888.
                                                                                                                                                                                                       97US-0059836.
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 01-JUL-1999 (first entry)
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Best Local Similarity 47.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001 (first entry)
                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                       WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO182 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AAX35204.
                                                                                                                 Homo sapiens.
                                                                                                                                                                                28-AUG-1998;
                                                                                                                                     WO9915664-A1
                                                                                                                                                                                                      24-SEP-1997;
                                                                                                                                                           01-APR-1999.
                                                                                                                                                                                                                                                    Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB00173;
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Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

Cor their agonists (preferably anti-PRO agonist antibody or a small

molecule minicking the biological activity of PRO polypeptide) are

useful in vitro or in vivo for inhibiting the growth of a tumour cell.

Compositions comprising the PRO polypeptides are useful for

inhibiting neoplastic cell growth and for treating cancer including

breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,

central nervous system cancer, melanoma and leukaemia in a mammal.

Central nervous system cancer, melanoma and leukaemia in a mammal.

Central nervous polypeptides are also useful for treating other disorders

cuch PRO polypeptides are also useful for treating other glandular,

macrophagal, epithelial, strongtal, hypothalamic and other glandular,

chiflammatory, angiogenic and immunologic disorders as well as being

useful for identifying agonists to PRO polypeptides by contacting the

custivity mediated by the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukeamia and for identifying compounds capable of inhibiting
                                                                                                                                                                                                                                                                                                                                                                'note= "cAMP and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin family signature
                                                                                                                                                                                                                                                                                96. 102
/note= "N-myristoylation site"
                                                                                                                                                    /note= "N-myristoylation site"
                                                                                                                                                                                                         /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "N-myristoylation site"
                                                                               1..18
∕label≈ Signal peptide
                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31; Fig 10; 133pp; English.
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99US-0144758.
99US-0145698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= I
125..131
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                                                                                                                                                                                                                            88..92
                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA54109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055319-A1.
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                                                                                                                      Modified-site
                                                                                                                                                                             Modified-site
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, anglogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A;
                                                  Gaps
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Surney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
Williams PM, Wood WI;
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43.2%; Score 57; DB 21; Length 135; 47.4%; Pred. No. 5.1; Live 5; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO182 protein sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                       AAB24391 standard; Protein; 135 AA.
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| 117 lqtlcctdgcsmtdlsalc 135
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99US-0141037.
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Watanabe CK, Williams PM,
                                                                                                       6 LSSSCCKWGCSKSEISSLC 24
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          Query Match 43.2
Best Local Similarity 47.4
Matches 9; Conservative
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N-PSDB; AAA77521.
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nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of zins3, a novel member of the insulin/relaxin family. The zins3 gene maps to human chromosome 1p31, a region that is correlated to a heritable form of non-insulin dependent diabetes mellitus (NIDDM). zins3 mRNA is not expressed
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115..135
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                                                                                                                                                                                      Query Match
Best Local Similarity 47.4%
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N-PSDB; AAA50150.
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June 27, 2002, 16:08:44; Search time 28.78 Seconds (without alignments) 20.369 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution: 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

SUMMARIES

		Description	1	Datont No. 5464/56	າຸ	۵, ۲	13,	13	Sequence 2, Appli	7	·		٠.	v (7			103		•	ý.	4,	'n	Sequence 2, Appli	7	4	. 2	֡֝֝֝֝֜֜֜֝֓֜֝֓֜֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֡֓֜֓֓֡֓֡֓֡֓֡	2 0	2 6	٠,	_	Patent No. 5464756
		ΙD	5464756-8	5464756-7	US-08-950-7208-6	US-08-905-267-13	- 00-214-00-	TO 00 001 TT	-/97	US-09-314-051-2	5464756-4	5464756-5	US-08-950-720A-2	TIS-08-442-248-2	7-047-746-00-01	7-CT9-0**-0-2	N	US-08-469-537A-103	5464756-1	US-08-673-789-2	TIC-08-443-560p-4	TC-00-407 447 0	7-0/4-604-00-60	05-08-484-219-2	US-09-158-706-2	PCT-US94-06997-4	5464756-2	US-08-443-568B-10	PCT-US94-06997-10	US-08-443-568B-12	DCT-11504-06007-12	1 0 0 0 1 1 0 0 1 1 1 7 1 1 1 1 1 1 1 1	2464/26-18
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28 52 39.4 164 6 5464756-20 29 52 39.4 185 3 US-08-950-720A-12 30 49 37.1 24 2 US-08-35-476-89 31 49 37.1 24 2 US-08-35-476-89 32 49 37.1 421 2 US-08-353-476-113 34 48 36.4 24 2 US-08-353-476-113 35 47.5 36.0 457 1 US-08-264-101-4 36 47.5 36.0 457 2 US-08-765-243-4 37 47.5 36.0 457 2 US-08-765-243-4 38 47.5 36.0 457 2 US-08-765-243-6 39 47.5 36.0 735 2 US-08-765-243-6 40 47.5 36.0 105-08-765-243-6 55 40 47.5 36.0 105-08-765-243-6 41 46 34.8 28 1 US-08-507-124-4 42 46 34.8 28 4 US-08-507-124-4 44 46 34.8 28 4 US-08-905-223-328 55 40 47-707-5428-6 56 40 47-707-5428-6 57 40 47-707-5428-6 58 40 40-07-707-5428-6 58 40 40-07-707-5428-6 58 40 40 40-707-707-5428-6 58 40 40 40 40 40 40 40 40 40 40 40 40 40	RESULT 1 5464756-8 ; Patent No. 5464756 ; Patent No. 5464756 ; JAMES A.; YANSURA, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, ; JAMES A.; YANSURA, DANIEL G. ; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE ; ISOLATION HUMAN RELAXIN ; NUMBER OF SEQUENCES: 42 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/908,766 ; FILING DATE: 01-JUL-1992 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 347,550 ; FILING DATE: 04-MAY-1989 ; SEQ ID NO:8: ; LENGTH: 24 5464756-8	Query Match 56.1%; Score 74; DB 6; Length 24; Best Local Similarity 55.0%; Pred. No. 0.0011; Matches 11; Conservative 5; Mismatches 4; Indels QY 5 GLSSCCKWGGSKSEISSLC 24	RESULT 2 5464756-7 ; Patent No. 5464756 ; Patent No. 5464756 ; JAMES A.; YANSURA, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, JAMES A.; YANSURA, DANIEL G. ; JAMES A.; YANSURA, DANIEL G. ; ISOLATION HUMAN RELAXIN ; NUMBER OF SEQUENCES: 42 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/908,766 ; FILING DATE: 01-JUL-1992 ; APPLICATION NUMBER: 347,550 ; RICHARD DATE: 04-MAY-1989 ; SEQ ID NO.7: LENGTH: 24 5464756-7	Query Match A7.7%; Score 63; DB 6; Length 24; Best Local Similarity 52.6%; Pred. No. 0.029; Matches 10; Conservative 4; Mismatches 5; Indels

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ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
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APPLICATION NUMBER: US/09/314,051
                                                                ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNCATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                STREET: 1201 CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastEd for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                              Sequence 6, Application US/08950720A; Patent No. 6046028; GENRRAL INFORMATION: APPLICANT: Conklin, Darrell C. APPLICANT: Lofton-Day, Catherine E. APPLICANT: Lok, Si APPLICANT: Lok, Si APPLICANT: Lok, Si APPLICANT: Jaspers, Stephen R. TTILE OF INVENTION: INSULIN HOWOLOG NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08905267; Patent No. 5959075; GENERAL INFORMATION:
APPLICANT: Lok, Si APPLICANT: CONklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Savislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : ||: ||| |:|||
| 117 LQALCCREGCSMKELSTLC 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LSSSCCKWGCSKSEISSLC 24
6 LSSSCCKWGCSKSEISSLC 24
                      6 MSIKCCIYGCTKKDISVLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.64
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  98102
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US-08-905-267-13
                                                                                                                      US-08-950-720A-6
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0; Gaps
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Sequence 13, Application US/09314051

Setent No. 6183991

GENERAL INFORMATION:
APPLICANT: Lok, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelborg, Anna C.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES. 1
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

46.2%; Score 61; DB 2; Length 213;
Best Local Similarity 50.0%; Pred. No. 0.43;
Matches 10; Conservative 2; Mismatches 8; Indels
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COMPUTER: IBM PC compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,267
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CLASSIFICATION:

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Gaps

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8; Indels

Mismatches

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9; Conservative
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  Matches
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0
                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Jelmberg, Atherine E.
APPLICANT: Jespers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
                                                                                                                                                                                                                                                                                                            46.2%; Score 61; DB 4; Length 213; 50.0%; Pred. No. 0.43; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 2
Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                  NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNICATION INFORMATION:
TELEPA: 206-442-6678
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/905,267
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NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08905267
Patent No. 5958075
GENERAL INFORMATION:
APPLICANT: Lok, Si
                                                                                                                                                                                                                                                                                                                                                                                                                          173 GYSEKCCLTGCTKEELSIAC 192
                                                                                                                                                                                                                                                                                                                                                                                     5 GLSSSCCKWGCSKSEISSLC 24
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INFORMATION FOR SEQ ID NO: 2:
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45.08;
      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        LENGTH: 213 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                        Query Match 46.2%
Best Local Similarity 50.0%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-314-051-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 200-----
TELEPHONE: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-905-267-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                       linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1201 E. CITY: Seattle
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APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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44.7%; Score 59; DB 4; Length 188;
Best Local Similarity 45.0%; Pred. No. 0.7;
Matches 9; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS, JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE TITLE OF STOLATION HUMAN RELAXIN
NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,051
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                            ; Sequence 2, Application US/09314051
; Patent No. 6183991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SAVAISHK, DEDORTH A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEPHONE: 206-442-6678
                                    163 GFADKCCAIGCSKEELAVAC.182
5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GFADKCCAIGCSKEELAVAC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TOPOLOGY: 1100-2-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-314-051-2
                                                                                                                                                                                                     GENERAL INFORMATION:
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STREET: 1202
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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JAMES A.; YANSURA, DANIEL G.
JAMES A.; YANSURA, DANIEL G.
JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
TISOLATION HUMAN RELAXIN
NUMBER OF SEQUENCES: 42
CUNRENT APPLICATION DATA:
PILING DATE: 01-JUL-1992
PRICATION HUMBER: 04-JUL-1992
PRICATION HUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 43.2%; Score 57; DB 6; Length 24; Local Similarity 47.4%; Pred. No. 0.18; A Conservative 3; Mismatches 7; Indels
                                                                                                                            43.9%; Score 58; DB 6; Length 22;
47.4%; Pred. No. 0.12;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08950720A; Patent No. 6046028
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                6 LSSSCCKWGCSKSEISSLC 24
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                                                                                                                                                                                                                                                   4 LSEKCCOVGCIRKDIARLC 22
                                                                                                                  Ouery Match
Best Local Similarity 47.4%
Local Similarity 47.4%
Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 120-
TTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                             5464756-5; Patent No. 5464756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LENGTH: 24
5464756-5
                                                         LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 9,
                                        ; SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:5
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47.4%; Pred. No. 0.93;
tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08442248
; Sequence 2, Application US/08442248
; Patent NO. 5759863
; GENERAL INFORMATION:
    APPLICANT: Garas, Ingrid W.
    APPLICANT: Winslow, John W.
    TITLE OF INVENTION: AL-1 Neurotrophic Factor
    NUMBER OF SEQUENCES: 18
    CORRESPENCE Genetech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: 5.25 inch, 360 Kb floppy disk IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTENT IN FOUNDATION OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,248
FILING DATE: 15-MAY-1995
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-CCT-1994
ATTORNEY AGENT INFORMATION:
NAME: TOTCHIA, TIMOLHY E.
REGISTRATION NUMBER: 920C4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFAX: 415/952-981
TELEFAX: 415/952-981
TELEFX: 910/371-7168
                ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
                                                                             REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LQTLCCTDGCSMTDLSALC 135
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LENGTH: 928 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-442-248-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 47.49
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                         US-08-950-720A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-442-248-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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STREET:
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43.2%; Score 57; DB 1; Length 928; 57.9%; Pred. No. 5.8; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FLING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY FACENT INFORMATION:
NAME: TOCCHIA, TIMCHAY E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
                                                                                                                                                                                                                                                                                APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: AGO Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.2%; Score 57; DB 1
57.9%; Pred. No. 5.8;
tive 3; Mismatches
                                                                                                                                                                                                                          ; Sequence 2, Application US/08440815; Patent No. 5798448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08486449
; Patent No. 6280732
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                       485 LSGSCCECGCGRA--SSLC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/225-8674
TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                               6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       485 LSGSCCECGCGRA--SSLC 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LSSSCCKWGCSKSEISSLC 24
                                      11; Conservative
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Matches 11; Conservative
                 Best Local Similarity
Matches 11; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                        US-08-440-815-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-486-449-2
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  Query Match
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 103, Application US/08469537A
Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OGT-1993
APPLICATION NUMBER: USSN 07/736,559
                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/486,449
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFBERNCE/POCKET NUMBER: P0920P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,952-9881
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                            SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 LSGSCCECGCGRA--SSLC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LSSSCCKWGCSKSEISSLC 24
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Best Local Similarity 57.99
Matches 11; Conservative
                                       California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                              USA
                                                                           94080
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US-08-469-537A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                          COUNTRY:
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5464756-1
; Patent No. 5464756
; Patent No. 5464756
; Patent No. 5464756
; JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
UNDHER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
PRICH APPLICATION NUMBER: 03/7/908,766
FILING DAPE: 01-70L-1992
PRICH APPLICATION DATA:
PRICH APPLICATION DATE: 1347,550
; FILING DATE: 04-MAY-1989
; SEQ ID NO.::
                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
43.2%; Score 57; DB 2; Length 1005;
Best Local Similarity 57.9%; Pred. No. 6.3;
Matches 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

42.4%; Score 56; DB 6; Length 24;
Best Local Similarity 42.1%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 7; Indels
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D. Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMONICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: June 27, 2002, 16:08:44 Job time: 193 sec
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 1005 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: TOPOLOGY: 11near
MOLECULE TYPE: protein
US-08-466-537A-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 LSGSCCECGCGRA--SSLC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LSSSCCKWGCSKSEISSLC 24
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 27, 2002, 16:09:27; Search time 36.01 Seconds (without alignments) 64.042 Million cell updates/sec

1 DVLAGLSSSCCKWGCSKSEISSLC 24 US-09-781-077-2_COPY_119_142 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	hopping trick the control of the con	relaxin - little s
SUMMARIES		
SUMM	A26463 A49739 BXRKOT B32201 B32201 B32201 B32201 B32201 B32201 B32201 B32201 B34905 B34936 B37327 B34936 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B37327 B4732 B4732 B4732 B4732 B4732 B4732 B4732	4067
DB		4
Length	20224488 10224488 108983 108983 108983 108983 10898 10898 1089 1089 1089 1089 1089 10	
% Query Match	0.00 0.00	!
Score	74 666 667 667 667 667 667 667 667 667 6	
Result No.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	

relaxin · guinea p hypothetical prote hypothetical prote surface protein 51 insulin 2 · toadfi	insulin - duckbill metallothionein - bombyxin A-1 homol insulin homolog 2 thionin variant Th Leydig insulin-lik thionin variant Th	
		ALIGNMENTS ments) (Spiny dogfish)
22.43	пппп	1 - spiny dogfish (fragments) s: Squalus acanthias (spiny
'	* ଫ ଫ ଫ ଫ ଫ ଫ	ALIGNMEN RESGLT 1 A26463 relaxin - spiny dogfish (fragments) C.Species: Squalus acanthias (spiny dogfish)
	48 36.4 33.2 T04851 48 36.4 444 2 T42979 47 35.6 50 1 INTO2	48 36.4 332 2 104851 48 36.4 444 2 142979 48 36.4 253 1 1729669 47 35.6 50 2 83835 47 35.6 60 2 83835 47 35.6 108 2 84358 47 35.6 108 2 843582 47 35.6 118 2 852549 47 35.6 136 2 852549

	iny dogfish (fragment qualus acanthias (spi vv-1988 #sequence_rev B26463; A26463. E.E.; Gowan, L.K.; sem. 161, 335-341, 19; action, purification, umber: A91179; MUD:: B26463. Pe: protein E',2-30 <bul> I. Source: ovary and control of the control o</bul>
ў п	Ouery Match 56.1%; Score 74; DB 2; Length 54; Best Local Similarity 55.0%; Pred. No. 0.0024; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Qy 5 GLSSSCCKWGCSKSEISSLC 24 : : : : : : : : : :
	RESULT 2 A49739 relaxin - horse (fragments) C;Species: Equus caballus (domestic horse) C;Species: Equus caballus (domestic horse) C;Apr-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995 C;Accession: B49739; A49739; A49739; A49739; A1991 R;Stewart, D.R.; Nevins, B.; Hadas, E.; Vandlen, R. Endocrinology 129, 375-383, 1991 A;Ritle: Affinity purification and sequence determination of equine relaxin. A;Reference number: A49739; MUID:91275796 A;Molecule type: protein A;Residues: 1-28 expres A;Molecule type: protein

Fri Jun 28 11:32:04 2002

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C; Species: Balaenoptera acuterostrata (minke whale, lesser rorqual)
C; Species: Balaenoptera acuterostrata (minke whale, lesser rorqual)
C; Date: 31-Uni-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C; Accession: B32201
K; Schwabe, C.; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
J. Biol. Chem. 264, 940-943, 1989
A; Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto A; Recession: B32201
A; Accession: B32201
A; Status: preliminary
A; Welceolle type: protein
A; Residues: 1-54 <SCH>
C; Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relaxin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 18-Jun-1999
C;Accession: A90934; A93187; A90205; A90196; S32313; S32312; A29796; A01615
C;Accession: Pudson, P.; Scanlon, D.; John, M.; Cronk, M.; Shine, J.; Tregear, G.; Ni
DNA 1, 155-162, 1982
A;Title: Porcine relaxin: molecular cloning and cDNA structure.
A;Reference number: A90934; MUID:83157118
                                                                                                                                                                                                                                                                                                   Cispecies: Balaenoptera edeni (Bryde's whale)
Cispecies: Balaenoptera edeni (Bryde's whale)
Cispecies: Balaenoptera edeni (Bryde's whale)
Cispecies: 31-ul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
Cispecies: 31-ul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
Cispecies: 132201; Heallesbach, E.E.; Heyn, H.; Yoshioka, M.
Bischwabe, C.; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
J. Biol. Chem. 264, 940-943, 1989
A; Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto
A; Reference number: A32201; MUID:89093167
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.9%; Score 58; DB 2; Length 54; 47.4%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                   Indels
                                   9
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Best Local Similarity 47.4%; Pred. No. 0.18; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 | || :|: || 36 LSEKCCQVGCIRKDIARLC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LSSSCCKWGCSKSEISSLC 24
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Best Local Similarity 47.4%
Local Similarity 47.4%
Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-54 <SCH>
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A;Molecule type: DNA
A;Residues: 1-182 <HAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-54 <SCH>C; Superfamily: insulin
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A;Title: On the primary and tertiary structure of relaxin from the sand tiger shark (Odd A;Reference number: A01616; MUID:82004703
A;Reference number: A01616
                                          C;Superfamily: insulin
C;Keywords: hormone; pyroglutamic acid
C;Keywords: hormone; pyroglutamic acid
C;Reywords: hormone; pyroglutamic acid
F;1-28,29-48/Promain: chain B #status experimental <CHB>
F;29-48/Domain: chain A #status experimental <CHB>
F;29-48/Domain: chain A #status experimental <CHB>
F;10-34/Domain: chain B #status experimental <CHB>
F;10-34/Domain: chain B #status experimental <CHB>
F;10-34,22-39,35-48/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1;2-19;21-44 <GGW>
R;Bullesbach, E.E.; Gowan, L.K.; Schwabe, C.; Steinetz, B.G.; O'Byrne, E.; Callard, I.P.
Eur. J. Blochem, 161, 335-341, 1986
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Int. J. Mass Spectrom. Ion Process. 111, 77-88, 1991
A;Title: Enzymatic digestion on the sample foil as a method for sequence determination
A;Reference number: A58793
A;Accession: BS8793
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C;Species: Phocoenoides dalli (Dall's porpoise)
C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relaxin - sand tiger (tentative sequence) (fragments)
C;Species: Odontaspis taurus (sand tiger)
C;Date: 01-Sep-1981 #sequence_revision 26-May-1995 #text_change 31-Mar-2000
C;Accession: A01616
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Matches 10; Conservative
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A;Molecule type: protein
A;Residues: 1-22 <WOO>
C;Superfamily: insulin
                             A; Residues: 29-48 <ST2>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Sep-1999
C;Accession: A01614
R;Hudson, P.; Haley, J.; Cronk, M.; Shine, J.; Niall, H.
Nature 291, 127-131, 1981
A;Title: Molecular cloning and characterization of cDNA sequences coding for rat rela A;Reference number: A01614; MUID:81197624
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F;36-173,48-186,172-177/Disulfide bonds: *status predicted
F;163/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predi
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C.Species: Canis lupus familiaris (dog)
C.Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C.Accession: B53879; A53879
R.Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A.Title: Purification and sequence determination of canine relaxin.
A.Reference number: A53879; MUID:93000391
A.Molecule type: protein
A.Residues: 1-35 SCSTE
A.Residues: 1-35 SCSTE
A.Residues: 1-35 SCSTE
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A.Residues: 36-59 Prodein
A.Residues: ASSTE ASST
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Pred. No. 0.53;
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42.18;
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A; Residues: 25-47, 'VW', 50 < SCH1>
R; Schwabe, C.; McDonald, J.K.
Biochen Biophys. Res. Commun. 74, 1501-1504, 1977
A; Title: Demonstration of a pyroqutamyl residue at the N terminus of the B-chain of por A; Rcontents: annotation; pyrrolldone carboxylic acid
A; Contents: annotation; pyrrolldone carboxylic acid
A; Reference number: A90196; MUD: 76231539
A; Reference number: A90196; MUD: 76231539
A; Molecule type: protein
A; Residues: 161-169, 'E', 171-182 < SCH>
B; Schwabe, C.; McDonald, J.K.
Science: 197, 914-915, 1977
A; Title: Relaxin: a disulfide homolog of insulin.
A; Reference number: A94245; MUD: 77236040
A; Contents: annotation: disulfide bonds
A;Cross-references: GB:K01088; NID:g164634; PIDN:AAA31114.1; PID:g164635
R;James, R.; Niall, H.; Kwok, S.; Bryant-Greenwood, G.
Mature 267, 544-546, 1977
A;Title: Primary structure of porcine relaxin: homology with insulin and related growth A;Reference number: A93187; MUID:77213067
A;Accession: A93187
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Kroinsday, T.; Takahara, H.; Sugawara, K.; Tagami, S.
Biol. Chem. Hoppe-Seyler 374, 203-210, 1993
A.Title: Endogenous heterogeneity of relaxin and sequence of the major form in pregnant
A.Reference number: S32312; MUID:93257096
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F:25-56,161-182/Product: relaxin #status experimental <RCB>
F:161-182/Domain: relaxin #status experimental <ACA>
F:161-182/Domain: relaxin chain A #status experimental <ACA>
F:25/Wodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F:34-169,46-182,168-173/Disulfide bonds: #status experimental
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A; Residues: 1-115, 'L',117-182 <HA2>
A; Residues: 1-115, 'L',117-182 <HA2>
A; Cross-references: GB:002792; NID:g164636; PIDN:AAA31115.1; PID:g164637
C; Comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation of C; Genetics:
A:Introns: 70/1
A:Introns: 70/1
C; Superfamily: insulin
C; Keywords: pyroglutamic acid
F; 1-24/Domain: signal sequence #status predicted <SIG>
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A.Residues: 161-182 <RO2>
RS.Haley, J.; Crawford, R.; Hudson, P.; Scanlon, D.; Tregear, G.; Shine, J.; Niall,
J. Biol. Chem. 262, 11940-11946, 1987
A.Title: Porcine relaxin. Gene structure and expression.
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A; Residues: 25-50, 'TWGR'; 161-182 <JAM>
B; Schwabe, C.; McDonald, J.K.; Steinetz, B.G.
Blochem Biophys. Res. Commun. 75, 539-510, 1977
A; Title: Primary structure of the B-chain of porcine relaxin.
A; Reference number: A90205; MUID:77157271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 LSEKCCOVGCIRKDIARLC 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 25-53 <KOH>
A; Accession: S32312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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receptor-like tyrosine kinase Ehk-1 - rat

1;

Gaps

7

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A; Status: preliminary
A; Molecule type: mRN,
A; Cross-references: EMBL:568026
A; Note: the authors translated the codon GAC for residue 170 as Glu
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C; Seywords: AFP; transmembrane protein
F; 675-941/Domain: protein kinase homology <KIN>
F; 683-691/Region: protein kinase ATP-binding motif
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subuitted to the EMBL Data Library, September 1999
A;Reference number: Z21691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin homolog ceinsulin-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Papio sp. (baboon)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: S42776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross references: EMBL: 227106; NID: 9415396; PIDN: CAA81622.1; PID: 9415397 C; Genetics:
A; Note: the authors translated the codon GAC for residue 170 as Glu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: rlx
S,Superfamily: insulin
C;Keywords: disulfide bond; hormone
F;1-24/Domain: relaxin chain A (fragment) #status predicted <RXA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.2%; Score 57; DB 2; Length 1005; 57.9%; Pred. No. 5; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.4%; Score 56; DB 2; Length 24; 42.1%; Pred. No. 0.36;
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A, Description: The sequence of C. elegans cosmid C17C3
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A;Accession: T1535
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Accession: S42776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596 LSGSCCECGCGRA--SSLC 612
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Best Local Similarity 42.1*
Best Local 8; Conservative
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Best Local Similarity 57.9%
Matches 11; Conservative
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A; Residues: 1-91 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-24 <EVA>
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                                                        A; Accession: S51602
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Richerence number: 847489
A. Descripțion: Expression and developmental regulation of EHK-1, a neuronal ELK-like rec
A. Reference number: 847489
A. Accession: 847489
A. Accession: 847489
A. Accession: 847489
A. Accession: 847489
A. Residus: preliminary
A. Molecule type: mrnA
A. Status: preliminary
A. Residus: 1-898 c/742>
A. Cispecfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
Cisuperfamily: protein kinase homology «KIN»
F; 568-834/Domain: protein kinase homology «KIN»
F; 568-834/Region: protein kinase ATP-binding motif
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C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C;Accession: S49015; S51602
C;Accession: S49015; S51602
C;Accession: S49015; S51602
C;Accession: S49015; S51603
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-jike tyrosine Kinase fam A;Reference number: S49015; MUID:94067777
C; Species: Rattus norvegicus (Norway rat)
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C; Accession: S51603
R; Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A; Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam A; Reference number: S49015; MUID:94067777
A; Accession: S51603
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-893 < MAIN.
A; Residues: 1-803 < MAIN.
A; Residues: 1-893 < MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL.868028
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
C;Keywords: ATP; transmembrane protein
F;563-829/Domain: protein kinase homology <KIN>
F;571-579/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%; Score 57; DB 2; Length 893; 57.9%; Pred. No. 4.6;
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3; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-1005 <MAI>
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 11; Conserve
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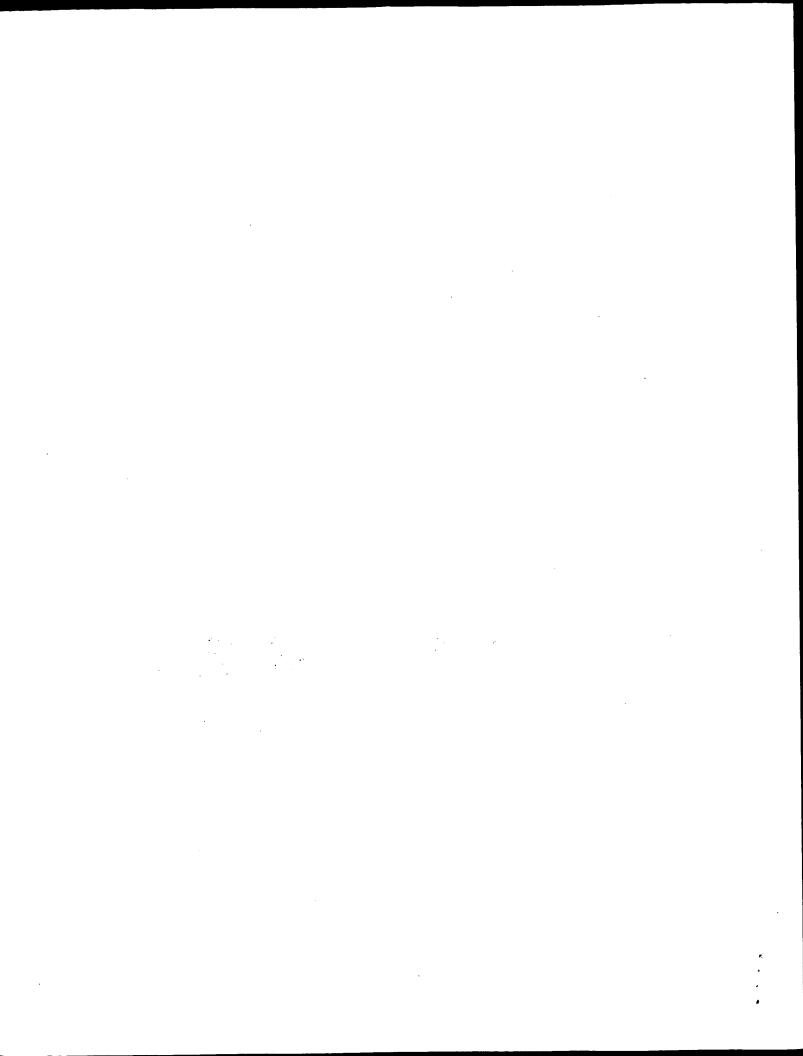
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Gaps

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relaxin precursor - rhesus macaque (Species: Macaca mulatta (rhesus macaque) (Species: Macaca mulatta (rhesus monor-relaxin 07-Sep-1990 #text_change 12-Jun-1998 (Species: Matagorian: A34936 (Species: Rocession: A34936 (Species: Rocession: A34936 (Species: A) 169-174, 1989 (Species: Bardocrinol. A) 169-174, 1989 (Species: Bardocrinol. A) 169-174, 1989 (Species: A) 1840 (Species: A) 184936 (Species: A) 184936 (Species: A) 184936 (Species: A) 185 (Species: A) 185 (Species: A) 185 (Species: A) 185 (Species: B) 185 (Species: Relaxin #status predicted (AMI))
A; Residues: 1-91 <DUZ>
A; Residues: BRL:U41279; NID:91086905; PID:91086914; PIDN:AAB52688.1; GSPDB:GN0G
A; Experimental source: strain Bristol N2; clone C17C3
C; Genetics:
A; Gene: C17C3.4
A; Map position: 2
A; Introns: 56/1
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                                                                                                                                                                                                                                          Query Match
42.4%; Score 56; DB 2; Length 91;
Best Local Similarity 41.7%; Pred. No. 1;
Matches 10; Conservative 5; Mismatches 9; Indels
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Search completed: June 27, 2002, 16:09:28 Job time: 212 sec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2002, 16:16:52; Search time 18.68 Seconds (without alignments) 49.747 Million cell updates/sec Run on:

US-09-781-077-2_COPY_119_142 Perfect score:

132 1 DVLAGLSSSCCKWGCSKSEISSLC 24 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:*

SUMMARIES

Ogyage mus musculu Ogysel homo sapien P58019 mus musculu Ogysel homo sapien P58019 mus musculu Ogysel homo sapien P1184 balaenopter P01348 sus Scrofa Ogysel homo sapien O18060 caenorhabdi P1988 macaca mula O60629 mus musculu P5548 procambarus P15131 locusta mig P51455 pan troglod P04090 homo sapien P0517. barley yell P81191 dasyatis sa P11952 raja erinac O9937. callithrix mus musculu mus musculu sus scrofa P11953 squalus aca P22969 equus cabal P01349 odontaspis homo sapien mesocricetu Description P81191 P11952 097937 P26371 Q64171 P47932 Q61554 RELX_ODOTA INL5_MOUSE INL6_HUMAN C59B_MOUSE INL6_RAT RELX_BALAC RELX_BALED RELX_PIG INLS_HUMAN RELX_CANFA RELX_CANFA EPAS_RAT EPAS_RAT EPAS_RAT ILG1_CAEEL RELX_MACMU ILG1_CAEEL RELX_MACMU EPAS_MOUSE MIL_MOUSE MIL_MOUSE MIL_MOUSE LIRP_LOCMI REL2_PANTR REL2_HUMAN RELX_DASSA RELX_DASSA INL3_CALJE KRUA_HUMAN RELX_MESAU V7K_BYDVP Query Score Match Length DB 186 1037 1037 1037 1857 191 75 221 195 63 81 63 64 131 164 177 41.7 40.9 40.5 39.4 39.4 39.4 39.4 339.4 339.4 339.4 Result . 9

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RESULT 2 RELX_HORSE

5 GLSSSCCKWGCSKSEISSLC

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P25127 P29453 P61453 P01338 P01338 Q94QY7 Q91010 P52727 P52722 P52722 P52723			ldri	О'В	from	SPECIES INKED BY	۲.				
		o4 AA. date) update)	<pre>Relaxin. Squalus acanthias (Spiny dogfish). Eukaryota; Ametazoa; Chordata; Craniata; Vertebrata; Chon Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus. 11.1797;</pre>	Steinetz B.G.,	fication, and the sequence of relaxin fracanthias)."; 161:335-341(1986).		ted. INSULIN/IGF/RELAXIN FAMILY		IN.	AIN. CARBOXYLIC ACID	1B7206773AD32A5B CRC64; Score 74; DB 1; Length 54; Pred. No. 0.00028; Mismatches 4; Indels
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6 LSSSCCKWGCSKSEISSLC 24

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Klonisch T., Ryan P.L., Yamashiro S., Porter D.G.,
"Partial complementary deoxyribonucleic acid cloning of equine relaxin messenger ribonucleic acid, and its localization within the equine placenta.";
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Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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L -> Q (IN REF. 2).
E5C9414303A838B8 CRC64;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-HOKKAIDO; TISSUE-Placenta;
Min K., Shicata K., Ogawa T.;
"Molecular cloning of equine preprorelaxin cDNA.";
J. Reprod. Dev. 42:171-178(1996).
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                     P22959; Q28907;
01-MUG-1991 (Rel. 19, Created)
01-MU97 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
182 AA.
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PIR; B49739; B49739.
HSSP; P01348; 4RLX.
InterPro; DR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
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                                                                                                                          Prorelaxin precursor (RXN).
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STANDARD;
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RELX_HORSE
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Pred. No. 0.011;
4; Mismatches 6; Indels
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Best Local Similarity 47.4%;
Matches 9; Conservative
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MEDILINE-62004703; PubMed=7274472; Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L.; Gowan L.K., the primary and tertiary structure of relaxin from the sand tiger shark (odontaspis taurus)."; FEBS Lett. 129:80-82(1981).
                                                                                                                                                                                                        Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5)
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
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6122F6604C660607 CRC64;
                                                                                                                                      11-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone.
164 LSHKCCYWGCTRKELARQC 182
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Best Local Similarity
Matches 10; Conserv
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-! FOUCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
DEVELOPMENT AND REGULATION.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
DISULRIDE BONDS (BY SIMILARITY).
-! TISSUE SPECIFICITY: HIGHEST EXPRESSION IN COLON WITH LOWER LEVELS
IN THYMUS. MELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                       MEDLINE-99389725; PubMed-10458910; Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E., Lok S., Jaspers S.; "Identification of INSL5, a new member of the insulin superfamily."; Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                               Hsu S.Y.; "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Moi. Endocrinol. 13:2163-2174(1999).
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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INSULIN-LIKE PROTEIN INSL5 B CHAIN
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CONNECTING PEPTIDE (POTENTIAL)
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Pred. No. 0.023;
4; Mismatches 5; Indels
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                                                                                           SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
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SWART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF133817; AAD29687.1; -.
EMBL; AF076971; AAD48089.1; -.
EMBL; AF054842; AAF09093.1; ALT_INIT.
EMBL; AF054843; AAF09094.1; -.
EMBL; BC010968; AAH10968.1; -.
MGD; MGI:1346085; Ins15.
                                                                                                                                                                                                                                 STRAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insulin family; Hormone; Signal.
 INSL5 OR ZINS3 OR RIF2 OR RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15524 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.6%
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
135
126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
135
                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AA;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49
115
                                                                                                            TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                         TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of INSL6, a new member of the insulin family that is expressed in the testis of the human and Rat.";
Biol. Reprod. 62.1593-1599(2000).
-!- FUNCTION: MAY HAVE A ROLE IN SPERM DEVELOPMENT AND FERTILIZATION.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20297000; PubMed-10819760;
Lok S., Johnston D.S., Conklin D., Lofton-Day C.E., Adams R.L.,
Jelmberg A.C., Whitmore T.E., Schrader S., Griswold M.D.,
Jaspers S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 A CHAIN
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN-LIKE PEPTIDE INSL6.
INSULIN-LIKE PROTEIN INSL6 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 C CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
JUNG, HUMAN STANDARD; PRT; 213 AM.
Q9Y581; Q9MS16;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last annotation update)
16-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL6 precursor (Insulin-like peptide INSL6 peptide INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.2%; Score 61; DB 1; Length 213; 50.0%; Pred. No. 0.066; Live 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> K (IN REF. 1).
8BA0976F660ACE8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000739; Insulin_IGF_relaxin.
Paran; PR00049; Insulin; 1.
SMART; SW00078; IIGF: 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF135824; AAF29604.1; -.
EMBL; AF156094; AAD39003.1; -.
MIM; 606414; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146
213 AA;
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                          INSL6 OR RIF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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Gaps

ö

5; Indels

52.6%;

117 LOALCCREGCSMKELSTLC 135

qq

6 LSSSCCKWGCSKSEISSLC 24

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Insulin-like peptide INSL6 precursor (Insulin-like peptide 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Balaenopteridae; Balaenoptera.
NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                                         SMART; SM00078; IlGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                              SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELX_BALAC
P11184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Relaxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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     QΣ
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                                                                                                                                                                                                                                                       Qian Y.-M., Qin X., Miwa T., Sun X., Halperin J.A., Song W.-C.;

Qian Y.-M., Qin X., Miwa T., Sun X.,

"Identification and functional characterization of a new gene encoding the mouse terminal complement inhibitor CD59.";

J. Immunol. 165:2528-2534(2000).

-I. FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK COMPLEX (MAC) ACTION. ACTS BY BINDING TO THE CB AND/OR C9 COMPLEX (MAC) ACTION. ACTS BY SINDING THE CB AND/OR C9 INCORPORATION OF THE ASSEMBLING MAC, THEREBY PREVENTING INCORPORATION OF THE OSMOLYTIC PORE (BY SIMILARITY).

-I. SUBJECTICITY: SPECIFICALLY IN TESTIS.

-I. SIMILARITY: CONTAINS: UUPAR/LYG DOMAIN.

MGD; MGI:1888996; CG559.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom; PDU0114; LU; 1.

SMART; SM00134; LU; 1.

PROSITE; PS00983; LY6_UPAR; FALSE_NEG.

Antigen; Glycoprotein; GPI-anchor; Signal.

SIGNAL 24 107 CD59B GIYCOPROTEIN.

TO REMOVED IN MATURE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPAR/LY6.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARLING GLCNAC.
N-LINKED (GLCNAC...) (POTENTIAL).
GPI-ANCHOR (BY SIMILARITY).
With SD619096AA9C9CEE CRC64;
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                   16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
16-007-2001 (Rel. 40, Last annotation update)
CD59B glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5; DB 1; Length 129; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LAGLSSSCCKWG-CSK-----SEISSL 23
                                                                                                                                                                                                                                                 MEDLINE=20405635; PubMed=10946279;
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001526; LY6_UPAR,
InterPro; IPR003632; Ly-6_CD59.
Pfam; PF00021; UPAR_LX6; 1.
Prodom; PP003128; Ly-6_CD59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14266 MW;
                    173 GYSEKCCLTGCTKEELSIAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.1%;
        5 GLSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
107
107
36
62
62
86
92
39
                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                   C59B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INL6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                             P58019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                              RESULT 6
C59B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INL6_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                           PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSULIN-LIKE PEPTIDE INSL6.
INSULIN-LIKE PROTEIN INSL6 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
INSULIN-LIKE PROTEIN INSL6 C CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSULIN-LIKE PROTEIN INSL6 A CHAIN
                                                                                                                                                          TISSUB-Testis; MEDLINE-20297000; PubMed-10819760; Lofton-Day C.E., Adams R.L., Lok S., Johnston D.S., Conklin D., Lofton-Day C.E., Adams R.L., Jelmberg A.C., Whitmore T.E., Schrader S., Griswold M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.7%; Score 59; DB 1; Length 188; 45.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50212AB3CE9982B3 CRC64;
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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BY SIMILARITY.
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RELX_PIG
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                               CHAIN
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                                                              MEDLINE-89093167; PubMed-2910872; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Schwabe C., Bullesbach E.E., Heyn H., Yoshioka M.; Cheacan relaxin: Isolation and sequence of relaxins from Balaenoptera acutorostrata and Balaenoptera edeni."; J. Biol. Chem. 264:940-943(1989).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBBUNT: HEDERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
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-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MANMALS.
-!- SUBBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
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Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
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-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
-1- SIMILARITY: DESCRIPTION TO THE INSULIN TO THE PROPERTY PROPERTY SMOOTOWN TO THE SIMIL T
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
HSP: 043201; A32201.
HSSP: A1348; 4RLX.
InterPro; IPR00049; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
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Pred. No. 0.055;
4; Mismatches
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01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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54
41
54
45
6099 MW;
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Insulin family; Hormone.
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Best Local Similarity 47.4%,
Local Similarity 47.4%,
Conservative
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[1]
SEQUENCE.
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SEQUENCE
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RELX_BALED
HD DT LAD DT LAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE-87308187; PubMed-2442155;
Haley J., Crawford R., Hudson P., Scanlon D., Tregear G., Shine J.,
Niall H.;
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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MEDLINE-77213067; PubMed-876374;
James R., Niall H., Kwok S., Bryant-Greenwood G.;
"Primary structure of porcine relaxin: homology with insulin and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-83157118; PubMed-6897721;
Haley J., Hudson P., Scanlon D., John M., Cronk M., Shine J.,
Tregear G., Niall H.;
"Porcine relaxin: molecular cloning and cDNA structure.";
DNA 1:155-162(1982).
                                                                                                      Length 54;
                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE OF 25-51.
MEDLINE=77157271; PubMed=851452;
Schwabe C., McDonald J.K., Steinetz B.G.;
Primary structure of the B-chain of porcine relaxin.";
Biochem. Biophys. Res. Commun. 75:503-510(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=76231539; PubMed=938497;
Schwabe C., McDonald J.K., Steinetz B.G.;
"Primary structure of the A chain of porcine relaxin.";
Biochem. Biophys. Res. Commun. 70:397-405(1976).
                                                           DB5535F8951F49BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Porcine relaxin. Gene structure and expression.";
J. Biol. Chem. 262:11940-11946(1987).
                                                                                                   Score 58; DB 1;
Pred. No. 0.055;
4; Mismatches
   RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                182 AA.
                              INTERCHAIN.
                  INTERCHAIN,
                                                                                                                                                                                                                                                              PRT;
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                                                                                                   43.98;
47.48;
54
41
54
45
6072 MW;
                                                                                                                                                          6 LSSSCCKWGCSKSEISSLC 24
                                                                                                                                                                                     36 LSEKCCOVGCIRKDIARLC 54
                                                                                  Ouery Match
Best Local Similarity 4/...
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related growth factors.";
Nature 267:544-546(1977).
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                   Prorelaxin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 161-182.
                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
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            DISULFID
DISULFID
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MIM; 606413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                       MEDILNE-78092399; PubMed-622170; Isaacs N.W., James R., Niall H., Bryant-Greenwood G., Dodson G.G., Evans A., North A.C.T.; Relaxin and its structural relationship to insulin."; Nature 271:278-281(1978).
-!-FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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30-MX-2000 (Rel. 39, Last sequence update)
30-MX-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
                                                                                                                                                      -i - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
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RELAXIN A CHAIN.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G -> GVWS (IN REF. 4).
WGRT -> TWGR (IN REF. 3).
S -> L (IN REF. 1).
Q -> E (IN REF. 6).
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4; Mismatches
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  "Relaxin: a disulfide homolog of insulin.";
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Pfam; PF00049; Insulin; 1.
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                                                                                                                                           - 1 - SUBCELLULAR LOCATION: Secreted.
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EMBL; J02792; AAA31115.1; -.
EMBL; A16593; CAA01295.1; -.
EMBL; A06652; CAA00600.1; -.
PIR; A01615; RXPG.
PIR; A29796; A29796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LSSSCCKWGCSKSEISSLC 24
              Science 197:914-915(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                               PDB; 1RLX; 15-OCT-94.
PDB; 2RLX; 15-OCT-94.
PDB; 3RLX; 15-OCT-94.
PDB; 4RLX; 15-OCT-94.
                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00078; IlGF;
                                    3D-STRUCTURE MODELING.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                  DISULFIDE BONDS
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                      DISULFIDE BONDS (BY SIMILARITY).
--- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN RECTUM WITH LOWER LEVELS
IN UTERUS AND ASCENDING AND DESCENDING COLON.
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                             Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E., Lok S., Jaspers S.;
"Identification of INSL5, a new member of the insulin superfamily.";
Genomics 60:50-56(1999).
                                                                                                                                                                                                                                                                                                                                                DEVELOPMENT AND REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
Canis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INSULIN-LIKE PEPTIDE INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSULIN-LIKE PEPTIDE INSL5 A CHAIN
                                                                                                                                                                                                                                                                                                                  -! - FUNCTION: MAY HAVE A ROLE IN GUT CONTRACTILITY OR IN THYMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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MEDLINE-99150177; PubMed=10026098;
MIDLINE-99150177; PubMed=10015098;
Klonisch T., Hombach-Klonisch S., Froehlich C., Kauffold J.,
Steger K., Steinetz B.G., Fischer B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.2%; Score 57; DB 1; Length 135; 47.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
98FFCB20E9C4BC1F CRC64;
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09TRM5, 09TRM9; 09N027;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                  SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                           MEDLINE=99389725; PubMed=10458910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF133816; AAD29686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LOTLCCTDGCSMTDLSALC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LSSSCCKWGCSKSEISSLC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 1
121 1
135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
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115
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                                                                                                                                                                                                   DISULTIDE DOUGO.

1 SUBCELLULAR LOCATION: Secreted.

1 TISSUE SPECIFICITY: Placenta; syncytiotrophoblast.

1 SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

1 SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
"canine preprorelaxin: nucleic acid sequence and localization within the canine placenta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murínae; Rattus.
                                                                                                                                                   -!- FUNCTION: Relaxin is an ovarian hormone that acts with estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-81197624; PubMed-7231533;
Hudson P., Haley J., Cronk M., Shine J., Niall H.;
"Molecular cloning and characterization of cDNA sequences coding for
                                                                                                                                                                   to produce dilatation of the birth canal in many mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                       Stewart D.R., Henzel W.J., Vandlen R.;
"Purification and sequence determination of canine relaxin.";
J. Protein Chem. 11:247-253(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.2%; Score 57; DB 1; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I -> S (IN REF. 2).
220BB0EC99DD302A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN.
                                                                                          MEDLINE=93000391; PubMed=1388669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin family; Hormone; Signal.
                 the canine placenta.";
Biol. Reprod. 60:551-557(1999).
                                                            SEQUENCE OF 26-60 AND 154-177.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF233687; AAF60302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 MSDKCCNVGCTRRELASRC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LSSSCCKWGCSKSEISSLC 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat relaxin.";
Nature 291:127-131(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prorelaxin precursor.
                                                                                                                                                                                                  DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                P01348; 4RLX
                                                                            TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maisonpierre P.C., Barrequeta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                               implications for physiological studies.";
Endocrinology 108:726-729(1981).
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN
TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (EPH homology kinase-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . ô
                                                John M.J., Borjesson B.W., Walsh J.R., Niall H.D.; "Limited sequence homology between porcine and rat relaxins:
                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%; Score 57; DB 1; Length 186;
47.4%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / SIMILARITY.
08BAEC79BCF0E80F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE. RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELAXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1005 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000739; Insulin_IGF_relaxin. Pfam; PF00049; Insulin; 1. SMART; SM00078; IIGF; 1. PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
MEDLINE=94067777; Pubmed=7504232;
[2]
SEQUENCE OF 23-57 AND 163-188.
MEDLINE-81090283; PUDMed=7004862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin family; Hormone; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                       EMBL; J00780; AAA42029.1; -. EMBL; V01264; CAA24578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20489 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
158
186
163
173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
9, Conserve
                                                                                                                                                                 DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                        PIR; A01614; RXRT.
HSSP; P01348; 4RLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 AA;
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DISULFID
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P54757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; PR000561; EGF-1ike.

InterPro; PR0001090; Ephrin_receptor.

InterPro; PR0001091; Ephrin_receptor.

InterPro; IPR0003961; Full.

InterPro; IPR003961; Full.

InterPro; IPR003961; Full.

InterPro; IPR001426; Receptor_tyr_kin_V.

InterPro; IPR00144; EPH_lbd; 1.

InterPro; IPR00144; INTERPRO; INTER
                                                                                                                                                                                                                                                                           tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND 6; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
-!- SIMILARITY: CONTAINS 1 SAM DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
                                                                                                               Lassmann H., Steck A.J.;
Expression and developmental regulation of Ehk-1, a neuronal
Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                  MEDLINE-95206467; PubMed-7898646;
Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). CYS-RICH. FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY). (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                       STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
                      SEQUENCE FROM N.A. (ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X78689; CAA55357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1005
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TRANSMEM
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RINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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Oncogene 10:897-905(1995).
--- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
---- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                 VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR
                                                                                                                                                                                                                                                                                                                                                                   RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
                                                                                                                                                                                                                                                                                                                                                                                            KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMMADPLAHTNY
TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
ISOFORM 3, ISOFORM 4, ISOFORM 5 AND
                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (Eph homology Kinase-1) (Receptor protein-tyrosine kinase HEK7).
EPHAS OR EHK1 OR HEK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                       GRRRTQGRGGG -> DADGPRAQASWCHARR (IN ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSCCECGCGRASSLCAVAHPSLIW -> R (IN
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MEDLINE-95206782; PubMed=7898931;
Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                              RESDPPTMACT -> G (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.2%; Score 57; DB 1; Length 1005; 57.9%; Pred. No. 0.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 170 | D -> E (IN REF. 2) | 170 | D -> E (IN REF. 2) | 170 | D -> E (IN REF. 2) | 170 | D -> E (IN REF. 2) | 170 | D -> E (IN REF. 2) | 170 | D -> E (IN REF. 2) | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 | 170 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1037 AA.
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOFORM 6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 LSGSCCECGCGRA--SSLC 612
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Best Local Similarity 57.9%
"...hes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                             358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPA5_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
PHOSPHORYLATION (AUTO-) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
              SÜBCELLULÄR LÖCATION: TYPE I MEMbrane protein.
ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
                                                                                       SIMILARITY: CONTAINS 1 SAM DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN
RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDZ-BINDING MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYS-RICH.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS: PRO0014; PRYTYPEIII.
PRINTS: PR00014; PRYTYPEIII.
PRINTS: PR00109; TYRKINASE.
ProDom: PD001495; ED11in_rcptor; 1.
SMART; SM00060; EN3: 2.
SMART; SM00060; EN3: 2.
SMART; SM00454; SAM: 1.
SMART; SM00459; TYKC; 1.
SMART; SM00419; TYKC; 1.
PROSITE; PS001186; EGF_2: UNKNOWN_1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; PROSITE; PS00109; PROTEIN_KINASE_DOM; PROSITE; PS00799; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00799; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; SMA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000561; EGF-like.
InterPro; IPR000199; Euk_pkinase.
InterPro; IPR000199; Euk_pkinase.
InterPro; IPR0001961; FN_III.
InterPro; IPR001962; FN_III_repeat.
InterPro; IPR001426; Receptor_tyr_kin_V.
InterPro; IPR001426; Receptor_tyr_kin_V.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF001401; EPH_lbd; 1.
Pfam; PF00041; fn3; 2.
Pfam; PF00061; fn3; 2.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP
                                                                                                                                                                                                                                                                                  EMBL; X95425; CAA64700.1; -.
EMBL; L36644; AAA74245.1; -.
HSSP; P29323; 1B4F.
    tyrosine phosphate.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
SCCECGCGRASSLCAVAHPILIW -> R (IN ISOFORM
                                                                                                                                             Gaps
                                                                                                                                             ;
;
                                                                                                              43.2%; Score 57; DB 1; Length 1037; 57.9%; Pred. No. 0.97; tive 3; Mismatches 3; Indels
                                                                                                                                            3; Indels
                                                                     1037 AA; 114784 MW; FC2C46C959AFB699 CRC64;
                                                                                                                                                                                                                                                    Search completed: June 27, 2002, 16:16:52 Job time: 486 sec
                                                                                                                                                                                        594 LSGSCCECGCGRA--SSLC 610
                                                                                                                                                                   LSSSCCKWGCSKSEISSLC 24
                                                                                                       Query Match
Best Local Similarity 57.9°
Matches 11, Conservative
 423
436
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 423
436
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597
 CARBOHYD
CARBOHYD
                             CARBOHYD
                                         VARSPLIC
                                                                     SEQUENCE
 FFFFF
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GenCore version 4.5
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OM protein - protein search, using sw model

June 27, 2002, 16:16:29 ; Search time 58.57 Seconds (without alignments) 70.887 Million cell updates/sec Run on:

US-09-781-077-2_COPY_119_142 Title: Perfect score:

132 1 DVLAGLSSSCCKWGCSKSEISSLC 24 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_unclassified:* sp_vertebrate:* sp_organelle:* sp_phage:* sp_plant:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* sp_rodent:* sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Optraf and escule	Obmite folds	Control terror Control	OC-040 Lamad	QSUOTS CAMEIUS Gro	nInosnu snu /50760	Uz8430 gorilla gor	Q28781 pongo pygma	Q9wla5 drosophila	Q9lv78 arabidopsis	O95vp6 leichmania	Odbive Described	Scales pseudollollas	U02189 Caenorhabdi	Q23141 caenorhabdi	0912w3 arabidoneia	Olderd's attachment	C14364 DOMO Sapien
	e l	09DEP8	D9TRG6	29MYK8	228787	0F026	040007	C28730	20400	220/01 00:11 a E	(SWIA)	8/178	295YP6	0XXH60	62189	10100	14162	09LZV3	14564	***
	DB	13	و	ی	ی د	ع ر		1 4			7									,
	Query Match Length DB ID	155	22	180	24	199	129	100	70	1 0	0 0	707	370	1159	399	000	0 10	448	169	i
æ	Query Match	47.7	43.9	43.2	42.4	42.4	39.8	39.4	39.4	.00		0.00	38.6	38.6	37.9	37.0		37.5	37.1	
	Score	63	58	57	26	26	52.5	52	52	5.15		7 .	75	51	20	0.5	9	4.7.0	49	
	Result No.	-	7	3	4	s	9	7	8	σ		7 -	77	12	13	14		CT	16	

ó

Gaps

; 0

Query Match 47.7%; Score 63; DB 13; Length 155; Best Local Similarity 47.6%; Pred. No. 0.02; Matches 10; Conservative 5; Mismatches 6; Indels

4 AGLSSSCCKWGCSKSEISSLC 24

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Q99119 mus musculu Q9wuh8 rattus norv Q88840 mus musculu Q95s27 drosophila Q90wx8 xenopus lae Q90x46 galago cras O65485 arabidopsis Q97x1 ateline her Q92577 homo sapien Q15061 homo sapien Q15061 homo sapien Q15061 homo sapien Q94711 paramecium Q9bx18 acropora mi Q9dy10 mus musculu Q9dy10 mus musculu Q9dy10 mus musculu Q9dy10 ans ansignio cras Q13203 ccenorhabdi Q16759 ccenorhabdi Q11m23 arabidopsis	ALIGNMENTS	Ogeres Og
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272 3672 3857 3857 3857 127 1127 1188 335 735 735 735 735 735 735 735 735 735		PRELIMINARY; PRT; (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last seq. (TrEMBLrel. 19, Last annoparties). Ta (Edible frog). Tetacoa; Chordata; Craniat rachia; Anura; Neobatractor; An.A. An.A. An.A. Branno M. An. Branno M. An.A. Branno M. An. Branno M.
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44.48; Pred. No. 0.21;

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Kohaska T., Takahara H., Sugawara K., Tagami S.;
Endogenous hererogeneity of relaxin and sequence of the major form in
pregnant sow ovaries.";
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Steger K., Huppertz B., Fischer B.;
"Nucleic acid sequence of feline preprorelaxin and its localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Felis silvestris catus (Cat).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnívora; Fissipedia; Felidae; Felis.
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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Hombach-Klonisch S., Klonisch T.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL; AF233688; AAF60303.1; --

HSSP; P04090; 6RLX.
                                                                                                                                                                                                                                                PLOST Chem. HOPPE-SEYLER 374:203-210(1993).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                            43.9%; Score 58; DB 6; Length 22; 47.4%; Pred. No. 0.018; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                        Interpro; IPR000739; Insulin_IGE_relaxin.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 22 AA; 2527 MW; F4DB25422449313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) RELAXIN R-III A CHAIN.
                         22 AA.
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SMART; SM00078; IlGF; 1.
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01-00T-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                          PRT;
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MEDLINE-99115216; PubMed-9915995;
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Biol. Reprod. 60:305-311(1999).
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PROSITE; PS00262; INSULIN; 1.
SEQUENCE 180 AA; 20360 MW;
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Matches 9; Conservative
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                          PRELIMINARY;
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                                                                                                             Sus scrofa (Pig)
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                                                                                                                                                    NCBI_TaxID=9823;
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                                                                                                                                                                                SEQUENCE
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                                         O9TRG6;
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                          Q9TRG6
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Q9MYK8
RESULT
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43.2%; Score 57; DB 6; Length 180;

Query Match

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                           Papio hamadryas (Hamadryas baboon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.

NCBI_TaxID=9557;
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Hombach-Rionisch S., Abd-Elnaeim M., Skidmore J.A., Leiser R.,
Fischer B., Klonisch T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Ruminant relaxin in the pregnant one-humped camel.";
Biol. Reprod. 62:839-846(2000).
-!- SUBCELLUIAR LOCATION: SECRETED (BY SIMILARITY).
--:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF254739; ARF67741.1; --
HSSP; P01348; IRLX.
InterPro. IPRO00739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                            42.4%; Score 56; DB 6; Length 24;
42.1%; Pred. No. 0.042;
tive 4; Mismatches 7; Indels
                Indels
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01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PREPROFEAXIN.
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01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
RELAXIN (FRAGMENT).
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                  4; Mismatches
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PROSITE; PS00262; INSULIN; 1.
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PROSITE; PS00262; INSULIN; 1.
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                                                                      163 SDRCCNVGCTRKELADLC 180
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Best Local Similarity 42.1.
Best Local 8; Conservative
                                                  7 SSSCCKWGCSKSEISSLC 24
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HSSP; P04090; 6RLX.
                8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Gaps

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8; Indels

Length 24;

Score 52; DB 6; Pred. No. 0.18;

39.4%; 33.3%;

6; Mismatches

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24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;
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                                                                                                    Best_Local Similarity 33.3
Matches 7; Conservative
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                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla
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-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                 42.4%; Score 56; DB 6; Length 199; 42.1%; Pred. No. 0.34; tive 5; Mismatches 6; Indels
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199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
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EMBL; AF292401; AALO4434.1; -.
SEQUENCE 129 AA; 14226 MW; 3B80648C8C30F635 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                               Created)
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MEDLINE=21363798; PubMed=11471050;
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                                                                                                              Conservative
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                                                                                         Best Local Similarity
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Best Local Similarity
Matches 12; Conserv
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SEQUENCE
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Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BERRELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
                                                                                                                                                                                                                                                Eukāryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                             39.4%; Score 52; DB 6; Length 24; 33.3%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 1 1 SEQUENCE 24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;
                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W1A5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                   24 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               868 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
24
                               24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00262; INSULIN; 1.
                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                   Pongo pygmaeus (Orangutan).
                   4 SALANKCCHVGCTKRSLARFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AGLSSSCCKWGCSKSEISSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SALANKCCHVGCTKRSLARFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 33.3
Matches 7; Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                  RELAXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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262 AA; 28098 MW; 5CD397647893BA11 CRC64;

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Bevangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA darris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., IDeyam C.,
RA Hannel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Markulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nakon K., Wuzny D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Saunders R.D., Pori V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Welistock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Welistock G.M., Weissenbach J.,
RA Phen X.H., Zhong F.N., Rubin G.M., Venter J.C.,
RA Phen X.H., Zhong F.N., Rubin G.M., Weissenbach J.,
RA Phen X.H., Zhong F.N., Rubin G.M., Weissenbach J.,
R. The genome sequence of Drosophila melanogaster.",
R. Science 287:2185-2285(2000).
R. Science 287:2185-2185(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA. CRROMOSOME 5, PI CLONE: WAK3.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.0%; Score 51.5; DB 5; Length 868; 52.6%; Pred. No. 7.6; tive 4; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              868 AA; 98470 MW; 4EA194B97F240D0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 262 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB019236; BAA97312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0034979; CG13569.
InterPro; IPR001283; SCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| || :|| 533 ASSCSDWGTTKSKEFANLC 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SSSCCKWGCSKS-EISSLC 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 52.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clones.";
DNA Res. 7:31-63(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00198; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=COLUMBIA;
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STRAIN-ATC. 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
Query Match 38.6%; Score 51; DB 10; Length 262; Best Local Similarity 47.6%; Pred. No. 2.8; Matches 10; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PREDICTED PROTEIN LM15-1.74, UNKNOWN FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A physical map of the Leishmania major Friedlin genome."; Geonne Res. 8:135-145(1998).
EMBL; ALIGO371; CAC5905-13; SEQUENCE 370; AR 38847 MW; 328C7ED7A2174886 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.6%; Score 51; DB 5; Length 370; 58.8%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                   PRT; 370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1159 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                            121 VLSGLASSLCQWASQVKKHSS 141
                                                                        2 VLAGLSSSCCKWGCSKSEISS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 AGHSSSSCKWICRNVQI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AGLSSSCCKWGCSKSEI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Leishmania major.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HYX0;
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                                                                                                                                                                                                                        Q95YP6;
                                                                                                                                                                                                   Q95YP6
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                                                                                                                                                                   RESULT 11
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L NATURE 406:959-964(2000).

C -1 SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

C -1 SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

EMBL; AE004749; AAG06659.1; -.

R InterPro; IPR0043594; HATPASS.C.

R InterPro; IPR004561; His_kina.

InterPro; IPR004561; His_kina.

InterPro; IPR004139; HIS_KIN_Sig.

InterPro; IPR004139; HIS_KIN_Sig.

InterPro; IPR004134; Na_Solut_symport.

R InterPro; IPR001014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
Complete protecome; Kinase; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                 38.6%; Score 51; DB 16; Length 1159; 35.7%; Pred. No. 12; Live 7; Mismatches 5; Indels 6
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                    1159 AA; 127452 MW; 1C4D145CE0E190CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFGM; PF00001; 7tm_1; 1.

PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.

PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.

SEQUENCE 399 AA; 45577 MW; 83FP18CF47A7CF88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL, 281520; CAB04223.1;
InterPro; IPR002106; Aa_trNA_ligase_II.
InterPro; IPR000276; GPGR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||::| :||1050 ILAGMNSLLSRWGCQVWTARSREECATL 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VLAGLSSSCCKWGC----SKSEISSL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                Pfam; PF02518; HATPase_c; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSR.
                                                                                                                                                                                                                                                                             SWART; SW00387; HATPASe_c; 1.
SWART; SW00091; PAS; 1.
SWART; SW00091; PAS; 1.
SWART; SW00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 50.00
Best Local Similarity 35.79
Watches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steward C.A.
                                                                                                                                                                                                                                                                                                                                                                      Transferase
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F31B9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        062189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
062189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           none;
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Length 399;

DB 5; 6.1;

Score 50; Pred. No.

37.9%; 59.1%;

Best Local Similarity

Query Match

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ς,
      Gaps
                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
      4,
                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
?;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.9%; Score 50; DB 5; Length 823; 61.1%; Pred. No. 12;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BRISTOL N2;
Miller N., Bradshaw H., Wu X., Gattung S.;
"The sequence of C. elegans cosmid W03Bl.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; U58753; AAC24437.1; -. InterPro; IPR002111; Cat_channel_TrpL. Hypothetical protein. SEQUENCE 823 AA; 95286 MW; 5AC484962DCDD7D4 CRC64;
                                                                                                                                                       or-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 95.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
(1.4)-EFRA-MANNAN ENDOHYDROLASE-LIKE PROTEIN.
T20L15_200.
      4;
                                                                                                                                   823 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA
   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                     STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                             343 DVAAGISSFCC-WLLPSFSKSE 363
                              1 DVLAGLSSSCCKW---GCSKSE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| ||| || : ||||
664 LTSGCCK--CSSTAISSL 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LSSSCCKWGCSKSEISSL 23
Matches 13; Conservative
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                               Q23141
Q23141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LZV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LZV3
                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                  023141
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                              δ
                                                         Pp
                                                                                                                                  δλ
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June 27, 2002, 16:08:08; Search time 73.16 Seconds (without alignments) 40.992 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   US-09-781-077-2_COPY_26_52
150

    protein search, using sw model

                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                               Scoring table:
                                                                      OM protein
                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                            Run on:
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SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT: (*SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:** (*SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:** (*SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:** (*SIDSI/gcgdata/hold-geneseqy-embl/AA1981.DAT:** (*SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1986.DAT:** (*SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:** (*SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:** (*SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1980.DAT:** (*SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1990.DAT:** (*SIDSI/gcgdata/hold-geneseqy
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RESULT AAG78114

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human insulin homo Asymmetry sequence Insulin-like pepti Human zins3 B chai Human Zins3 protei Pro-insulin-like p PRO182 polypeptide Human PRO182 prote Human insulin fami PRO182 Polypeptide Human EST encoded
SUMMARIES	AAGY8114 AAR96006 AAY95773 AAY95773 AAM97925 AAM01961 AAB00173 AAB24391 AAB24391 AAY95770 AAY8328
DB	22 20 20 21 20 21 21 22 22
% Query Match Length DB ID	142 300 135 135 135 135 135 135 135
& Query Match	100.0 58.0 54.7 54.7 54.7 54.7 54.7 54.7 54.7 54.7
Score	150 822 822 822 823 823 823 823 823
Result No.	1 2 3 4 4 7 7 7 10 11 11

Human PRO182 polyp Human immunostimul Human anglogenesis Relaxin-like facto Mouse Zins3 protei Mouse Lins1 fami Human Rif partial Prorelaxin B-chain Human relaxin B-ch	Ubiquitin-relaxin Ubiquitin-relaxin H2 prorelaxin gene H2 prorelaxin dedu Sequence of human Sequence of human Sequence of human Sequence of human		Human gene 2 encod Caenorhabditis ele C. elegans insulin Human secreted pro Human gene 2 encod Prolrelaxin fragme Human polypeptide Rat Zins2 testis-s
2 AAU12309 2 AAB20110 3 AAB20110 3 AAW07863 4 AAW07863 1 AAS95771 1 AAS965772 AAR64894 2 AAR64894 1 AAR05208	AAA	A A	AAE0604 AAB0614 AAY6565 AAX8715 AAE0613 AAR6490 AAO0324
135 22 135 22 135 22 31 18 135 21 46 21 29 16 29 16 46 11	4 0 4 10 10 10 10 10	0 0 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	
44400004444 4440000744	444444 CCCC	4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
112 82 113 82 114 76 115 76 117 75 118 71 119 71 21 71	CCCCCCC	~ ~ • • • • • • • • • • • •	<u> </u>
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ALIGNMENTS

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Human; insulin; zins4; relaxin; chromosome 19p13.11; cytostatic; antifertility; vasotropic; reproductive disorder; prostate disorder; handext disorder; kidney disorder; gonadal development; pregnancy; pubertal change; menopause; ovarian cancer; testicular cancer; ovulation; polycystic ovarian syndrome; contractile tissue; cardiovascular disease; birth control; impotence; myocyte; endothelial cell; osteoblast; blood pressure; muscle tension; osmotic balance; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                34..47
/label= B.chain_consensus_sequence_region
/label= Given in SEQ ID NO 3*
37..41
/label= B_chain_conserved_motif
                                                                                                                                                                                                                                                                                                    /note= "Zins4, claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                         /label= B_chain
/note= "Claimed in claim 1"
                                                                              Human insulin homologue polypeptide Zins4.
                                                                                                                                                                                                                                                          1..25
/label= signal_peptide
26..142
/label= mature_protein
                                                                                                                                                                                                                                             Location/Qualifiers
AAG78114 standard; Protein; 142 AA.
                                                    (first entry)
                                                                                                                                                                                                                  Homo sapiens.
                                                   21-NOV-2001
                         AAG78114;
                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                           Region
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New insulin homologue polypeptide having homology to relaxin family, designated zins4 and zins4 polynucleotide, useful for diagnosing, preventing, treating reproductive, prostate, heart and kidney disorders
                                                      /note= "Cleavage site at the junction of the C peptis and the A chain with a conserved RXXR motif"
                                                                                                       /label= A_chain_consensus_sequence_region
/note= "Given in SEQ ID NO 4"
/note= "Given in SEQ ID NO 5"
                                                                               /label= A_chain
/note= "Claimed in claim 2"
                                55..114
/note= "Claimed in claim 3"
                                                                                                                                                                                                                                                                                          Claim 6; Page 72-73; 79pp; English.
                         /label= C_peptide
                                                                                                                                                                                                            Holloway JL, Lok S, Jaspers SR;
                                                                                                                                                              09-FEB-2001; 2001WO-US04199.
                                                                                                                                                                              10-MAR-2000; 2000US-0523346
                                                                                               ..142
                                               .118
                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                        119..142
                                                                                                                                                                                                                            WPI; 2001-582454/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142 AA;
                                                                                                                                                                                                                                     N-PSDB; AAH79088
                                                                                                                               WO200168862-A1
           Cleavage-site
                                                 Cleavage-site
                                  Region
                                                                         Region
                                                                                                 Region
                   Region
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The invention relates to an isolated insulin homologue zinst having chomology to the relaxin family. The zinst gene, located on chromosome composition and a chain comprising amino acid protein, where the Linst polypeptide comprises a B chain and A chain comprising amino acid residues 26.52 and comprises a B chain and A chain comprising amino acid residues 26.52 and comprises a B chain and A chain comprising amino acid residues 26.52 and comprises are useful; in applications for enhancing fertilisation during proteins are useful in applications for enhancing fertilisation during casisted reproduction in humans and animals and in therapies for treating reproductive disorders. Zinst protein is useful in treating reproductive, comprise to its activity. Zinst protein is useful in treating reproductive, collines which respond to the zinst-stimulated pathway and to identify inhibitors of its activity. Zinst polypeptides and modulators of the cinhibitors of its activity. Zinst polypeptides and modulators of the collines which respond to the zinst-stimulated pathway and to identify inhibitors of its activity. Zinst polypeptides and modulation, outation, collective collines are also mother reproductive functions including pathological conditions in ovary. Detection of zinst polypeptides in the serum or tissue biopsy of a patient is useful for diagnosing ovarian cancer. The molecules are also useful for treating dysfunction associated with control, treating importance or other male reproductive dysfunction, collutes and also useful for treating dysfunction, development and/or maturation of ovarian cells, myocytes, endothelial cells, osteoblasts in collution pirth, for promoting growth, differentiation, development and/or maturation of ovarian cells, myocytes, endothelial cells, reproductive directions and fertilisation. The polypeptide is also useful as a modulator of blood pressure, muscle tension and osmotic
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Gaps

; 0

8 RLCGREFIRAVIFTCGGSRW 27

δλ

ö

Gaps

; 0

Query Match
Best Local Similarity 100.0%; Score 150; DB 22; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.3e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0;

Conservative

Query Match Best Local Similarity Matches 14; Conserv

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AAR AAR95999-R96006 represent the asymmetry sequences of target binding assemblies (TBA) of the invention. The TBA is recognised by the target binding region (TBR) of a probe of the invention. The Probe of the tortion contains a TBR, a booster binding region (BBR), and an contion a trachment (OSA). The TBA contains at least one optional support or attachment (OSA). The TBA contains at least one contains a support or attachment (NSA), and optionally a linker sequence, an asymmetry sequence, an unclear localisation signal sequence, and an OSA. The assembly sequence and asymmetry sequences are responsible for the folding and association of the NARs. The NARs are reported from NF kappa-B, FBL, TATA, human papillomarius (HPV) ETR and Tat binding units. The LINKer sequence is an oligopeptide, which does not interfere with NAR function, but provides stability and control over the spacing of the NAR correct from the rest of the TBA. The OSA is an attached support or indicator, or other means of localisation of the probe. The probe can be used in a method for detecting or localishing a specific target nucleic acid of specificity. The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic of specificity. The method is highly sensitive, and has a high degree of specificity. The method can be used for detecting specific nucleic of other nucleic acid containing systems, including bacteria and viruses.
                                                                                                                                                                                                                                                                                                                Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1; TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus; HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence; nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe nucleic acids, target binding assemblies, etc - for detection and localisation of specific nucleic acid sequences, esp. HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.0%; Score 87; DB 17; Length 40; 70.0%; Pred. No. 1.9e-05; tive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 108-109; 172pp; English.
                      26 raapygvrlcgrefiraviftcggsrw 52
27
                                                                                                                                                   AAR96006 standard; peptide; 40 AA.
  1 RAAPYGVRLCGREFIRAVIFTCGGSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0353476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weininger S;
                                                                                                                                                                                                                                        19-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                   Asymmetry sequence #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENE POOL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-287199/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weininger AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09617956-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                              AAR96006;
                                                                                                             N
                                                                                                                                 AAR96006
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Homo sapiens.
                          AAY95773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
           Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents insulin-like polypeptide (pro-ILP)

chain B peptide. The ILP protein is expressed in the colon and uterus,

and is a member of the insulin/IGF family. The immature pro-ILP

comprises a 135 amino acid sequence, which is processed into the mature

form which comprises an A chain and a B chain linked by disulfide bonds.

The C-peptide of pro-ILP exists as a separate peptide after processing

of pro-ILP. The ILP protein is useful in treatment of disorders related

to neurophysiological function affecting fluid homeostasis, electrolyte

concurrence are acidate characteristic activity and collagen

conforming the methods can be used for diagnosing a physiologic or

pathologic condition of the uterus, colon or other ILP-expressing cell

or tissue and for diagnosis and screening of modulators and therapeutics.

conce: the present sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; electrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.7%; Score 82; DB 20; Length 30;
66.7%; Pred. No. 7.5e-05;
ilve 2; Mismatches 5; Indels
                                                                                                                                                                                  Insulin-like peptide (pro-ILP) chain B peptide.
                                                                                        AAY01963 standard; Peptide; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY95773 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page -; 75pp; English.
9 rlcgrdlirafiylcggtrw 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 vrlcgleyirtviyicassrw 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0059836.
                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US17888
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX35207
                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                            01-APR-1999.
                                                                                                                       AAY01963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY95773
ID AAY9
                                                                             AAY01963
                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a peptide from the B chain of human zins3 (see AAY95770). The peptide was used to immunize guinea Pigs, rabbits and chickens to generate antibodies for zins3, which were used in assays to determine the tissue distribution and cell expression of zins3. Zins3 is a novel member of the insulin/relaxin family whose gene maps to a region of human chromosome ip associated with non-insulin dependent diabetes mellitus (NIDDM). Zins3 polynuclectides and polypeptides can be used to diagnose disorders associated with abnormal expression of zins3 and to identify polymorphisms that result from mutations in the zins3 gene. The invention provides methods for identifying abnormalities in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression that are a factor in causing, or predisposing, a person to some defect in glucose metabolism, such as NIDDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 82; DB 21; Length 31; 66.7%; Pred. No. 7.8e-05; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                 Zins3; insulin; relaxin; human; diagnosis; NIIDM; non-insulin dependent diabetes mellitus; immunogen.
                                                                      Human zins3 B chain peptide immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW37925 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 34; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 vrlcgleyirtviyicassrw 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FEB-2000; 2000WO-US03515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0250125.
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07-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7 ies 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-558220/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Zins3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 AA;
                                                                                                                                                                                                                                                                                                      WO200047776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1999;
                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                     17-AUG-2000.
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δy qq 98WO-US17888 97US-0059836.

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Colon and uterus expressed insulin-like polypeptide, useful in the treatment of disorders related to neurophysiological function
                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-254713/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX35204
                          WO9915664-A1.
                                                                                                                                                28-AUG-1998;
                                                                                                                                                                                                              24-SEP-1997;
                                                                                     01-APR-1999.
                                                                                                                                                                                                                                                                                                                                              Gurney A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB00173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Zins3 protein is an insulin homologue protein. Polynucleotide molecules taken from its gene can be introduced into a cultured cell using an expression vector. The cell will express an insulin homologue polypeptide encoded by the polynucleotide. The polypeptides can also be expressed by introducing the polynucleotides into the germline of a nonhuman animal. The polypeptides can be used to identify and isolate receptors for zins3. Antibodies and antagonists of the polypeptides can be used for treating disease associated with extracellular matrix and vessels. The antibodies may also be used in the diagnosis of diseases associated with the polypeptide, such as reproductive diseases associated with the placenta and uterus, gastrointestinal diseases, and placental and colon pathology. Antagonists against the polypeptide may also be used to treat diseases such as preclampsia, premature labour, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insulin-like polypeptide; pro-ILP; ILP; insulin/IGF family; A chain; B chain; C chain; neurophysiological function; fluid homeostasis; alectrolyte homeostasis; cardiovascular function; blood pressure; somatic; cardiac ionotropic activity; cardiac chronotropic activity; collagen deposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - used to, e.g.
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Pred. No. 0.00034;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin homologue polypeptide(s) and antagonists – used tc
treat pre-eclampsia, premature labour and Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaspers SR, Lofton-Day CE, Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro-insulin-like peptide (pro-ILP).
                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01961 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 64-65; 81pp; English.
                                                                                                                                                      "C-peptide"
                                                                                        "B chain"
                                                                                                                                                                                                                 /note= "A chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.7%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.79
                                                                                                                                                          /note= "C-
115..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-251285/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV29150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1996;
                                                                                                                                                                                                                                                                                      W09816635-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conklin DC,
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                                                              Peptide
                                                                                                                            Peptide
                                                                                                                                                                                          Peptide
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The present sequence represents an insulin-like polypeptide (pro-ILP). The protein is expressed in the colon and uterus, and is a member of the insulin/IGF family. The immature pro-ILP comprises a 135 amino acid sequence, which is processed into the mature form which comprises an A chain and a B chain linked by disulfide bonds. The C-peptide of pro-ILP exists as a separate peptide after processing of pro-ILP. The ILP protein is useful in treatment of disorders related to neurophysiological function affecting fluid homeostasis, electrolyte homeostasis, cardiovascular function, blood pressure, somatic or cardiac hontropic activity, cardiac chronotropic activity and collagen deposition. The methods can be used for diagnosing a physiologic or pathologic condition of the uterus, colon or other ILP-expressing cell or tissue and for diagnosis and screening of modulators and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; volvarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder; anglogenic disorder; immunologic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82; DB 20; Length 135;
Pred. No. 0.00034;
2; Mismatches 5; Indels
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/note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..18
/label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Claim 5; Fig 6B; 75pp; English.
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66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 AA;
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Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides

or their agonists (preferably anti-PRO agonist antibody or a small
molecule minicking the bloiogical activity of PRO polypeptide) are
useful in vitro or in vivo for inhibiting the growth of a tumour cell.
Compositions comprising the PRO polypeptides are useful for
inhibiting neoplastic cell growth and for treating cancer including
breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder,
central nervous system cancer, melanoma and leukaemia in a mammal.
The PRO polypeptides are also useful for treating other disorders
such as neuronal, glial, astrooytal, hypothalamic and other glandular,
inflammatory, angiogenic and immunologic disorders and
inflammatory, angiogenic and immunologic disorders as well as being
useful for identifying agonists to PRO polypeptides by contacting the
colypeptide with a candidate molecule and monitoring biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukeamia and for identifying compounds capable of inhibiting growth of neoplastic cells
                                                                   /note= "cAMP- and cGMP-dependent protein kinase 113\dots117
                                                                                                     /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                         /note= "Casein kinase II phosphorylation site"
              /note= "Casein kinase II phosphorylation site"
                                                                                                     121...136
/label- Insulin family signature
125..131
                             96..102
/note= "N-myristoylation site"
                                                                                                                                                     /note= "N-myristoylation site"
127..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 31; Fig 10; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                        99WO-US20594.
99WO-US21090.
99WO-US23089.
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99US-0145698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-638201/61.
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Modified-site
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26-JUL-1999;
08-SEP-1999;
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05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999
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                                           Gaps
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 54.7%; Score 82; DB 21; Length.135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
Query Match
Best Local Similarity 66.7'
Matches 14; Conservative
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useful for preventions, distributed actus actus and control of propertions useful for prevention, disponsing and treating disponsing a cardiovascular, endothelial or angiogeneis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and disponsis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.

135 AA;

Sequence

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26 vrlcgleyirtviyicassrw 46
7 VRLCGREFIRAVIFTCGGSRW 27
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diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; anglogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
                                                                                   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                Baker KP, Ferrara N, Gerber H, Hillan KJ, Godd:
Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
Williams PM, Wood WI;
                                                                Human PRO182 protein sequence SEQ ID NO:16.
        AAB24391 standard; Protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 72; Fig 8; 315pp; English.
                                                                                                                                                                                                                                                                                                                                              99WO-US21090.
99WO-US21547.
99WO-US23089.
99US-0162506.
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99US-0123957
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                                             07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-412154/35.
N-PSDB; AAA77521.
                                                                                                                                                   WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ,
                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski PJ,
Watanabe CK,
                                                                                                                                                                                         30-NOV-1999;
                                                                                                                                                                       08-JUN-2000.
                                                                                                                                                                                                                                                                    14-MAY-1999
                                                                                                                                                                                                                                                                                                                   01-SEP-1999
                                                                                                                                                                                                                                                                                                                            08-SEP-1999
                            AAB24391;
AAB24391
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members of the insulin family, cleavage at the C-terminus of the B-chain and at the N-terminus of the A-chain, resulting in removal of the C-peptide. Cysteine residues at positions 29 and 41 (B-chain) and 121 and 135 (A-chain) are capable of associating through cysteine bridges and forming disulfide-bonded molecules.

135 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin/relaxin family. The zins3 gene maps to human chromosome insulin/relaxin family. The zins3 gene maps to human chromosome to pal, a region that is correlated to a heritable form of non-insulin dependent diabetes mellitus (NIDDM). zins3 mRNA is not expressed in detectable announts in healthy tissue, indicating that the zins3 colynucleotide is a candidate marker for a disease state and/or a specialized cell type. zins3 polynucleotides and polypeptides can be used to diagnose disorders associated with abnormal expression of the zins3 protein, and to identify polymorphisms that result from mutations in the zins3 gene. In particular, the invention provides methods for identifying abnormalities in expression that in glucose metabolism, such as NIDDM. Processing of the mature in glucose metabolism, such as NIDDM. Processing of the mature zins3 protein involves cleavage at the C-terminus of the signal peptide and, based on predicted structural homology with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying mutations in human chromosome 1p31, preferably a zins3 gene mutation, comprises using an insulin/relaxin family member (designated zins3), useful for diagnosing non-insulin dependent diabetes
                                     Gaps
                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of zins3, a novel member of the
54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaspers SR, Whitmore TE, Conklin DC, Lofton-Day CE,
                                                                                                                                                                                                                                                                                                                            Zins3; insulin; relaxin; human; diagnosis; NIIDM;
non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ..22
'label= Signal_peptide
                                                                                                                                                                                                                                                                                            Human insulin family homologue zins3.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 44-45; 51pp; English.
                                                                                                                                                                                          AAY95770 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23..48
/label= B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C-chain
115..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115..135
/label= A-chain
                                                                       7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                          |||||| |:|| ||: | |||
26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-1999; 99US-0198248.
12-FEB-1999; 99US-0250125.
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                                                                                                                                                                                                                                                            (first entry)
                                     14; Conservative
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                     Best Local Similarity
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                                                                                                                                                                                                                          AAY95770;
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                       Matches
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Gaps
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                                                                                                                                                                                                                 Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "cAMP and cGMP dependent protein kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                             88..92
/note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M,
54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034;
tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Insulin family signature sequence"
                                                                                                                                                                                                                                                                                                                                     /note= "N-myristoylation site"
52..58
                                                                                                                                                                                                                                                                                                                                                                  'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                 /...102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                             AAY83228 standard; Protein; 135 AA.
                                                            |||||| |:|| ||: | ||| || 26 vrlcgleyirtviyicassrw 46
                                               7 VRLCGREFIRAVIFTCGGSRW 27
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                                                                                                                                                                          16-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..136
              Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            113..117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                                                                                                                                                                               PRO182 Polypeptide.
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                                                                                                                                                   AAY83228;
    Query Match
                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                        human.
                                                                                                        RESULT 10
                                                                                                                  AAY83228
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Gaps

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54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels

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26 vrlcgleyirtviyicassrw 46
                                                                                                                                                  7 VRLCGREFIRAVIFTCGGSRW
                                                                             Query Match
Best Local Similarity 66.75
        protein of the invention.
                                        135 AA;
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                                        Sequence
                                                                                                                                                                                                                                                                                                AAU12309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith V,
        SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomator. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel
             Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                            polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia.
                                                                                                        Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen R, Asundi V;
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                       54.7%; Score 82; DB 21; Length 135; 66.7%; Pred. No. 0.00034; Live 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 1068-1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human EST encoded protein SEQ ID NO: 1558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                           Claim 14; Figure 10; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM24033 standard; Protein; 135 AA
                                                                                                                                                                                                                                                                                                                                       26 vrlcgleyirtviyicassrw 46
                                                                                                                                                                                                                                                                                                                      7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001; 2001WO-US02687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                          Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH98692.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM24033;
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate, cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beresini M, Deforge L, Desnoyers L, Filvaroff E, G;
ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
AAU12309 standard; Protein; 135 AA
                                                                     Human PRO182 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2000; 2000W0-US00277.

11-FEB-2000; 2000W0-US00376.

11-FEB-2000; 2000W0-US03441.

18-FEB-2000; 2000W0-US04342.

22-FEB-2000; 2000W0-US04414.

24-FEB-2000; 2000W0-US04414.

24-FEB-2000; 2000W0-US04914.

24-FEB-2000; 2000W0-US05601.

21-MAR-2000; 2000W0-US05601.

21-MAR-2000; 2000W0-US05632.

30-MAR-2000; 2000W0-US08377.

21-MAR-2000; 2000W0-US08439.

17-MAY-2000; 2000W0-US13705.

22-MAY-2000; 2000W0-US13705.
                                                                                                                                                                                                                               01-DEC-2000; 2000WO-US32678.
                                                                                                                                                                                                                                                                                                                                        99WO-US30911.
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99WO-US30095,
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2000WO-US00277.
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                                             24-OCT-2001 (first entry)
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                                                                                                                                                                               WO200140466-A2.
                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                             09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
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02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                      of T-1ymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polypuclectides encoding
                                                                                                                                              AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumnours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumnour necrosis factor-alpha (TNF-alpha) from human blood the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
        Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammallan tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "cAMP- and cGMP-dependent protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96..102
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Signal_peptide
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                                                                                                              Claim 12; Fig 276; 813pp; English.
                                                                         lung, breast, prostate, cervical
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26 vrlcgleyirtviyicassrw 46
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Matches 14; Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 135 AA;
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The present sequence is that of PRO182 (UNQ156), a novel human continuous protein encoded by CDNA (see AAF30052) isolated immunomodulator protein encoded by CDNA (see AAF30052) isolated from a uterine CDNA library. The invention provides Polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO182. Claimed composition of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response in a mammal, or increasing the proliferation of T-lymphocytes on mammal in response to an antigon. Claimed compositions of T-lymphocytes in a mammal in response to an antigon. Claimed compositions of T-lymphocytes on agonist antibody or an antagonist have the opposite effect. A claimed method for treating an immune related disorder, involves administering the PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, content antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, synemic acternosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune harmolytic syndromic autoimmune thrombooytopaenia, thyroiditis, diabetes mellitus, inflammatory bowel disease (lampeliated diseases (such as autoimmune mediated continuomatous hepatitis, sclerosing cholangitis, billiary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (lampel and cranplantation associated diseases (such as such as sethma, allergic chiming a control of seases (such as asthma, allergic chiming a compound capable of inhibiting the expression of the PRO polypeptide, vectors, host cells and compound capable of inhibiting the expression or the level of expression of the process.
                                                                                                                                                                                                                                                                                       Gurney AL;
                                                                                                                                                                                                                                                                                     Godowski PJ, Gurney AI
Tumas D, Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes -
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                                                       /note= "insulin family signature"
            /note= "N-myristoylation site"
121..136
                                                                                                                                                                                                                                                                                       Goddard A,
Pitti RM,
                                                                                                                                                                                                                                                                                       Ashkenazi AJ, Baker KP, Fong S,
Hillan KJ, Mark MR, Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Fig 6; 127pp; English
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                                                                                                                                                                         15-MAR-2000; 2000WO-US06884.
                                                                                                                                                                                                                99US-0144758.
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Best Local Similarity 66.7%
125..131
                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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                                                                                           WO200105972-A1.
Modified-site
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                                      Peptide
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or additional procession in a PRO gene, or the expression level of a PRO gene within a protein a protein a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular issue; treating a cardiovascular, endothelial or angiogenic clisorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a
                                                                                                                                                                      Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardidovascular disorder; endothelial disorder; angiogenic disorder; atheroscolerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; crown sidisease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or anglogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                        Human angiogenesis-associated protein PRO182, SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ, Baker KP, Ferrara N, Gerber H,
Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Ma
Paoni NF, Pitti RM, Watanabe CK, Williams PM,
                                  AAB53072 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 69; Fig 18; 293pp; English.
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99WO-US21090.
99WO-US21547.
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99US-0144758.
99US-0145698.
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99WO-US12252
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                                                                                                  28-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                               Homo sapiens.
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08-SEP-1999;
15-SEP-1999;
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26-JUL-1999;
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14-MAY-1999
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                                                                    AAB53072;
RESULT 1
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Goddard A;

Mark MR, Ma M, Wood WI;

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PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antigonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as therefore or stroke. Sosteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential invaries. The present sequence represents a PRO protein of the invaries.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Forms disulphide bond with A chain Cysll" 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Forms disulphide bond with A chain Cys24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular disease; neurodegenerative disease;
neurological disease; sinus bradycardia; depression; hair loss;
collagen; scleroderma; fibronectin; insulin.
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                     54.7%; Score 82; DB 22; Length 135; 66.7%; Pred. No. 0.00034;
tive 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW07863 standard; peptide; 31 AA.
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Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwabe C, Unemori E;
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                                                                                                                                                                                                                                                                                                        135 AA;
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                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                       invention.
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Claim 1; Page 48; 60pp; English.

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The sequences given in AAW07862-63 represent the A and B chains of relaxin-like factor (RLF). RLF displaces bound relaxin tracer from the receptor to which it is bound. The RLF can be used to treat relaxin treatable conditions, esp. cardiovascular disease, neurocorrection treatable conditions as a proposition of degenerative or neurological disease, sinus bradycardia, depression, collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled or large in binding assays, and for relaxin receptor mapping. RLF collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin. RLF can be radiolabelled collagen (e.g. scleroderma) or fibronectin and insulin.

ANA SQ Sequence 31 AA;

Query Match S5.0%; Pred. No. 0.00056; Indels 0; Gaps 0; RRCGREFIRAVIFTGGSRW 27 | Hismatches 5; Indels 0; Gaps 0; Hill | Hill: | Hill | Hill | Hill: | Hill | Hill
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Search completed: June 27, 2002, 16:08:09 Job time: 278 sec

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June 27, 2002, 16:08:44; Search time 28.78 Seconds (without alignments) 22.915 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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	Description	Patent No. 5464756	NO. 546475	00 apr	S	4	14,	9	2	Sequence 5, Appli	7	5	No.	ce 14,	Sequence 14, Appl	10,			NO.	ce 1	13	90		٦		NO.	No. 546475	App
SUMMARIES	ID	5464756-16	5464756-15	US-08-353-476-92	-08-950-720A-	-08-484	US-08-950-720A-14	-950	US-08-443-568B-2	Н	-0699	5464756-11	5464756-10	US-08-443-568B-14	PCT-US94-06997-14	US-08-443-568B-10	PCT-US94-06997-10	5464756-18	5464756-20	o	US-08-950-720A-13	0	9	US-09-158-706-1	5464756-14	5464756-9	5464756-12	US-08-443-568B-12
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	Score	116	102	87	83	16	16	75	7.1	71	7.1	71	71	71	7.1	71	71	71	7.1	71	71	69	89	9	67	57	22	23
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53 35.3 150 5 PCT-US94-06997-12 53 35.3 188 4 US-08-905-267-2 51 34.0 35 6 544756-13 49 32.7 213 4 US-09-314-051-2 49 32.7 213 4 US-09-314-051-3 48 32.0 603 4 US-09-314-051-3 47 31.3 29 1 US-09-097-889-23 47 31.3 29 1 US-09-097-889-23 47 31.3 50 6 543515-16 47 31.3 50 6 543615-16 47 31.3 50 6 543615-16 47 31.3 50 6 543615-16 47 31.3 70 1 US-08-435-25-1 47 31.3 70 1 US-09-147-035-1 47 31.3 70 1 US-09-166-165-166-166-169-169-169-169-169-169-169-169	Appl 100 pp 11 100 p		.		0;
53 35.3 150 5 PCT-US94-06997-12 Seque 53 35.3 188 2 40.8-90-24.2677.2 Seque 53 35.3 188 2 40.8-90-24.2677.2 Seque 53 35.3 188 2 40.8-90-24.267.2 Seque 49 32.7 213 2 13-60-90-24.051.13 Seque 49 32.7 213 2 13-60-90-24.051.13 Seque 47 31.3 31.7 577 6 535275-9 Pertent 47 31.3 36 544951.7 Pertent 47 31.3 36 544951.7 Pertent 47 31.3 36 544951.7 Pertent 47 31.3 50 6 5448513-2 Pertent 47 31.3 70 1 105-07-64-611-2 Seque A7 31.3 30 31.3 50.00-07-61-2 Seque A7	2, April 12, 12, 13, 14, 14, 14, 14, 14, 14, 14, 14, 14, 14		Č,		Gaps
53 35.3 150 5 PCT-US94-06997-12 53 35.3 188 4 2 US-08-995-267-2 51 34.0 13 5 6 5464756-13 49 32.7 213 2 US-08-9905-267-13 49 32.7 213 4 US-09-314-051-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.6 6 5489517-2 47 31.3 3.7 0 1 US-09-9180-522-5 47 31.3 70 1 US-09-9180-522-17 47 31.3 70 1 US-07-654-611-2 47 31.3 70 1 US-07-654-611-2 47 31.3 70 1 US-07-9180-522-17 48 DATE: O1-UUL-1992 48 A64756 48 AND MAN RELAXIN 58 ESCURENCES: 42 58 64756 59 ESCURENCES: 42 59 ESCURENCES: 42 59 ESCURENCES: 42 59 ESCURENCES: 42 50 ESCURENCES: 42 50 ESCURENCES: 42 51 US-07-97-98-766 50 ENFERTION NUMBER: 347.550	uence uence uence nt Nc uence uence uence uence uence		.;0		0;
53 35.3 150 53 53 150 53 35.3 150 53 35.3 188 53 35.3 188 64 9 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 47 31.3 7 577 64 7 31.3 3 36 64 7 31.3 3 57 6 64 7 31.3 3 67 64 7 31.3 3 70 14 7 31.0 8	S S S S S S S S S S S S S S S S S S S	L.; WILKINS, OR THE	Length ; Indel	L.; WILKINS, OR THE	Length 29 ; Indels
53 35.3 150 53 53 150 53 35.3 150 53 35.3 188 53 35.3 188 64 9 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 48 49 32.7 213 47 31.3 7 577 64 7 31.3 3 36 64 7 31.3 3 57 6 64 7 31.3 3 67 64 7 31.3 3 70 14 7 31.0 8	PCT-US94-06997-12 US-08-955-267-2 US-09-314-051-2 546475-13 US-08-955-267-13 US-09-314-051-13 US-09-097-889-23 535255-9 US-08-4135-25-1 5470721-2 548517-2 548517-2 US-07-963-329A-2	ALIGNMENTS ; VANDLEN, RICHARD 1 AND COMPOSITIONS FG //908,766	Score 116; DB 6; Pred. No. 1.6e-10 ; Mismatches 7	Ω ^{[ii}	
28 53 35.3 150 53 35.3 188 53 35.3 188 51 51 49 32.7 213 49 32.7 213 49 32.7 213 49 32.7 213 49 32.7 213 49 32.7 213 55.15 47 31.3 32 47 31.3 35.3 35 67 47 31.3 37 67 47 31.3 37 67 47 31.3 37 67 47 31.3 37 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 47 31.3 70 67 67 ENVENTION PROOFILE G. THILD DATA PAPLICATION HUMAN RELAXIN WINDER OF SEQUENCES: UGNERIT APPLICATION HUMBER: UNIVERSENT PAPLICATION DATA PAPLI	RU40044040404044111	LS J CESS 7: 13/07 992 17,55	38; 48; 48; 111 38RW	.s J.	# # 00
28 53 35.3 36.3 36.3 37.3 38.3 38.3 38.3 38.3 38.3 38.3 38	1188 1188 1188 213 22 213 32 32 33 34 70 70 70 70	DENN. IEL G. N: PROC AXIN AXIN CON DAT/ BER: 1 JOHA: 34	77. y 86. rvative VIFTCGC	, DENNI IEL G. AXIN TO AXIN TO AXIN TO ES: 42 ES: 42 DN DATA JUL 19 JUL 19 DATA: 34	v.at
28 53 53 53 53 53 53 53 53 53 53 53 53 53	35.3 345.3 345.3 35.3 35.3 31.3 31.3 31.3 31.3 31.3 3	4756 HENNER RA, DAN NVENTIO MAN REL SEQUENCY I LON NUM ATE: 04	nilarit Conse SREFIRA SREFIRA	1756 HENNER HENNER AAN DAN WENTION WENTION TO TICATIC TICATIC TICATIC NUM WEEL OF TICATIC NUM WEEL OF TICATICN NUM WEEL OF TICATICN NUM WEEL OF TICE TICATICN NUM WEEL TICE TICATICN NUM WEEL TICE TICATICN NUM WEEL TICE TICATICN NUM WEEL TICATICN NUM WEEL TICE TICATICN NUM WEEL TICE TICATICN TICE TICATICN TICATIC	h Similarity 17; Conser
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RESUL	2 2 9 2 9 3 9 3 9 9 9 9 9 9 9 9 9 9 9 9	SUI 547 ate AME IS	Query Best Match Qy Db	RESULT 2 5464756 15 ; Patent No. APPLIC; JAMES A.; Y ; ISOLATIC ; ISOLATIC ; ISOLATIC ; PREN ; PRICH ; PRICH ; PRICH ; SEQ ID NO. ; SEQ ID NO. ; SEQ ID NO. ; SEQ ID NO. ; LENG	Query M Best Lo Matches

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STREET: 1201 Eastlake Avenue East
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                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                        Seattle
                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                            98102
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                                                           COUNTRY:
                                         STATE:
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                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Weininger, Arthur M
APPLICANT: Weininger, Arthur M
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.0%; Score 87; DB 2; I 70.0%; Pred. No. 3.6e-06; tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st St., Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CONKLIN, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lok, Si.
APPLICANT: Jaspers, Stephen R.
ITILE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: GP-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 92: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08950720A Patent No. 6046028
                                                                                                                                                               Sequence 92, Application US/08353476 Patent No. 5871902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZymoGenetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                          6 GVRLCGREFIRAVIFTCGGSR 26
                                             9 GIKLCGREFIRAIIFACGGSR 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 70.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ON.
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                                                                                                                         RESULT 3
US-08-353-476-92
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Gaps
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GENERAL INFORMATION:
APPLICANT: Schwabe, Christian
APPLICANT: Unemori, Elaine
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                         US/08/950,720A
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 VRLCGLEYIRTVIYICASSRW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.78;
                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,43
                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 54.7;
Best Local Similarity 66.7;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
Diskette
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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Gaps
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0
                   50.7%; Score 76; DB 3; Length 101; 55.0%; Pred. No. 0.00036; tive 4; Mismatches 5; Indels
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52.4%; Pred. No. 0.00068;
tive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR *****
CIARGO DATE:
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Lofk, Si.
APPLICANT: Jaspers, Stephen R.
TILLE OF INVENTION: INSULIN HOMOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                           Sequence 6, Application US/08950720A Patent No. 6046028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08443568B; Patent No. 5759807; GENERAL INFORMATION:
APPLICANT: Breece, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION:
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VRLCGREFIRAVIFTCGGSRW 27
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                                                                                              8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                 32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sawislak, Deborah A REGISTRATION NUMBER: 37,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 amino acids
                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 206-442-667
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-950-720A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                        Best Local Similarity Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1201 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                         Query Match
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                                                                                                                                                                                                                                                                                                          50.7%; Score 76; DB 2; Length 31; 55.0%; Pred. No. 0.00011; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIANE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,720A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08950720A
Patent No. 6046028
GENERAL INFORMATION:
APPLICANT: Conklin, Darrell C.
APPLICANT: Lofton-Day, Catherine E.
APPLICANT: Jaspers, Stephen R.
TTYLE OF INVENTION: INSULIN HOWOLOG
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICALL.
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
NAME: 37,438
       REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842
TELECHMONICACION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEFAX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                       S KLCGHHFVRALVRVCGGPRW 27
                                                                                                                                                                                                                                                                                                                                                                                    8 RLCGREFIRAVIFTCGGSRW 27
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POPOLOGY: linear
MOLECULE TYPE: No. 6046028e
US-08-950-720A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 101 amino acids
                                                                                                                                                                     TYPE: amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLGGY: unknown

MOLECULE TYPE: protein

US-08-484-219-4
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.0°
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-950-720A-14
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TOPOLOGY: unknown
                     SOFTWARE:
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PCT-US94-06997-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.3%; Score 71; DB 1; Length 29; 57.1%; Pred. No. 0.00056; tive 3; Mismatches 6; Indels
                                      APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/443,568B FILING DATE: 22-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7842-037
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Schwabe, Christian
APPLICANT: Oremori, Elaine
TITLE OF INVENTION: THEREOF
TITLE OF SEQUENCES: 6
COMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/080,354
Hayenga, Kirk
Rindersknecht, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION 1735

APPLICATION NUMBER: 08/080,35.
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B.
REGISTRATION UNUMBER: 30,605
REFERENCE/COCKET NUMBER: 7842
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08484219
Patent No. 5911997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 57.19
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                         New York
: U.S.A.
                                                                                                                                                                                       New York
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                                                                                                                                                                                                                                                  10036
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                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-484-219-5
                       APPLICANT:
                                                                                                                                                                                                         STATE:
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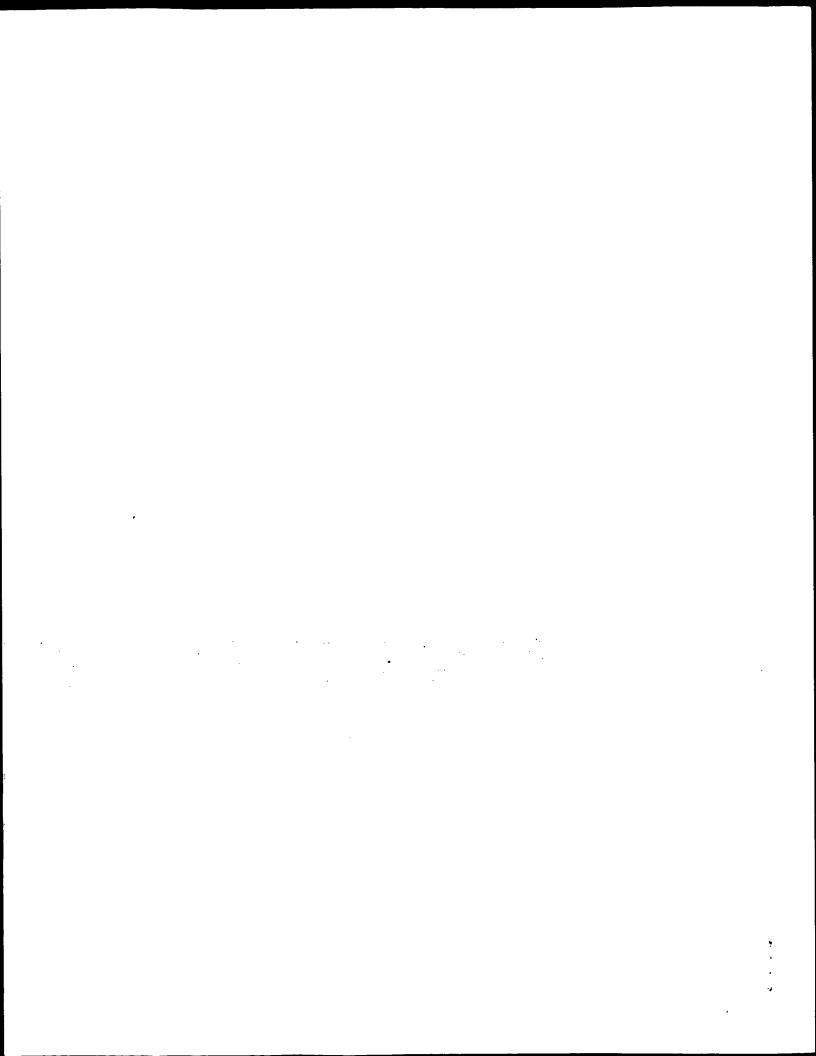
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDERESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06997
FILING DATE: 20-JUN-1994
                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7842-025-228
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  7842-040
                                                                      US/08/484,219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9406997 GENERAL INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842-
TELECOMMUNICATION INFORMATION:
TELEPAN: 415-854-3660
TELESA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATERISTICS:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISKATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7842:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELER: 66141 PENNIE
TELEX: 61141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
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                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                       29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-219-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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GENERAL INFORMATION:
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5464756-11
;Patent No. 5464756
; APPLICANT: HENNER, DENNIS J.;VANDLEN, RICHARD L.;WILKINS,
                                                                                                                                                                    Query Match
47.3%; Score 71; DB 5; Length 29;
Best Local Similarity 57.1%; Pred. No. 0.00056;
Matches 12; Conservative 3; Mismatches 6; Indels
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47.3%; Score 71; DB 6; Length 33;
Best Local Similarity 57.1%; Pred. No. 0.00064;
Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JAMES A.; YANSURA, DANIEL G.
TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE
J. ISOLATION HUMAN RELAXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,766
FILING DATE: 01-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 347,550
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08443568B Patent No. 5759807
                                                                                                                                                                                                                                                                                                                                                      7 VRLCGREFIRAVIFTCGGSRW 27
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; MOLECULE TYPE: protein PCT-US94-06997-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 32
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US-08-443-568B-14
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                                                             APPLICANT: Vandian, Richard
APPLICANT: Vandian, Richard
APPLICANT: Daniel, Yansura
ITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genericch, Inc.
APPLICANT: Genericch, Inc.
APPLICANT: 460 Point San Bruno Boulevard
APPLICANT: South San Francisco, California
APPLICANT: United States of America
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/443,568B FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7842-037
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PCT-US94-06997-14
Sequence 14, Application PC/TUS9406997
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
APPLICANT: Breece, Tim
APPLICANT: Hayenga, Kirk
APPLICANT: Rindersknecht, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 57.1'
Matches 12; Conservative
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OPERATING SYSTEM:
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STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Breece, Tim
APPLICANT: Hayenga, tirk
APPLICANT: Rindersknecht, Ernst
APPLICANT: Wandlen, Richard
APPLICANT: Vandlen, Richard
APPLICANT: Vandlen, Richard
APPLICANT: Daniel, Yansura
TITLE OF INVENTION: Process for Producing Relaxin
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUWINY: U.S.A.
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MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,568B
FILING DATE: 22 MAY 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 22,227
REFERENCE/DOCKET NUMBER: 7842-025-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acids
                                                                                             APPLICATION NUMBER: PCT/US94/06997 FILING DATE: 20-JUN-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08443568B Patent No. 5759807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/080,354
FILING DATE: 21-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,605
REFRENCE/DOCKET NUMBER: 7842
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VRLCGREFIRAVIFTCGGSRW 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
PCT-US94-06997-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
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US-08-443-568B-10
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2002, 16:09:27; Search time 36.01 Seconds (without alignments) 72.047 Million cell updates/sec Run on:

US-09-781-077-2_COPY_26_52 150 Title: Perfect score: Sequence:

1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	QI	A26463	RXRKOT	A29543	B53024	A53024	S42786	S42784	S42783	A44559	A60982	S42778	B32201	S48082	A53879	I56451	A34936	A58793	A32201	RXPG	S42781	T27987	A49739	147053	T29014	RXRT	A48586	S42785	T10897	S71427
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	Length	54	44	64	131	131	166	57	166	185	185	57	54	185	59	33	185	31	54	182	33	106	48	143	112	186	988	24	187	448
dР	Query	77.3	64.0	58.0	50.7	20.0	48.0	47.3	47.3	47.3	47.3	42.0	40.7	40.7	40.0	38.0	38.0	37.3	36.7	36.7	36.0	35.3	34.7	34.7	34.0	34.0	34.0	33.3	33.3	
	Score	116	96	87	16	75	72	71	71	71	7.1	63	19	61	09	57	57	26	55	55	54	53	52	52	51	51	51	20	50	20
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449 2 2 1106 2 2 15 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	S41647 T27989 T474466 T47444 INEN INFI INFO T27988 F95115 F95105 G85746 G85746 G85746 A49194 A48827	ALIGIST STATES STATES SCHWADE BE AND THE AND T		r e	equence) 1 tiger) 1 sion 26 1be, C.; 1ry stru 32004703
30 50 33.3 449 31 49.5 33.0 106 32 33 49.5 33.0 106 33 49.5 33.0 105 34 49.5 33.0 105 35 49.5 33.0 105 36 49.5 33.0 107 37 49.3 2.7 107 38 49.3 2.7 107 38 49.3 2.7 107 38 48.5 32.3 375 48 32.0 140 42 48 32.0 140 42 48 32.0 140 43 32.0 140 44 32.0 140 45 48 32.0 140 47 48 32.0 140 5.Buchem. 161, 335-341, 5.Bullesbach, E.E. Gowar, E.P. 5.Buchem. 161, 335-341, 5.Bullesbach, E.E.; Gowan, E.R. 6.Suchem. 161, 335-341,		nent (Spi rev (C.; 19 (On,	10 TE # 20 C 11		_ 25 € 50 ···
30 50 33.3 31 49.5 33.0 32 49.5 33.0 33 49.5 33.0 33 49.5 33.0 33 49.5 33.0 33 49.5 33.0 33 49.5 33.0 35 49 32.7 36 49 32.7 37 49 32.7 38 48.5 32.3 39 48.5 32.3 39 48.5 32.3 40 48 32.0 41 48 32.0 42 48 32.0 44 48 32.0 45 Eur. J. Biochem. 161, 47 Hitle: Isolation, purce: he amino-term Arithe: Around and a source: C, Superimental Source: H; 13-41,25-54,40-45/DI Best Local Similarit Matches Local Similarit Matches 19; Conse Oy 6 GVRLCGREFIRA Db GIKLCGREFIRA Db GIKLCGREFIRA C, Species: Odontaspis A; Hill: On the primar A; Reference number: A; Reference number: A; Reference number: A; Residues: 1; 2-1; 21: 21: 21: 21: 21: 21: 21: 21: 21: 21:	44 402 322 323 323 405 405 405 405 405 405 405 405	hh (fragr mthias mthias 26463 26463 Wan, 1.1 Wan, 1.1 1179; Mt	inal res	y 86.4 rvative VIFTCGGS	
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	0 11 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	RESULT A26463 C. Date: C. Date: C. Acces R. Bulle Eur. A. Title A. Acces A. Acces A. Moleci	A, Note: A, Access A, Resid A, Exper C, Super C, Super C, F; 1-30, F; 1-1 Mod F; 13-41,	Best Match SULT	KAKKOI C.SPECIK C.SPECIK C.ACCESS C.ACCESS R.GOWEN, FEBS LET A.Title: A.Refere A.Refere A.Residu A.Residu R.Bulles

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A; Cross-references: GDB:230307; OMIM:146738
                        A; Map position: 19p13.2-19p12
A; Introns: 64/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Raja erinacea (little skate)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 16-Feb-1997
C;Accession: A29543; Schwabe, C.; Callard, I.P.
Biochem. Biophys. Res. Commun. 143, 273-280, 1987
A;Tille: Relaxin from an oviparous species, the skate (Raja erinacea).
A;Reference number: A29543; MUID:87156758
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A; Residues: 1-131 <BUS>
A; Cross-references: GB:X73637
R; Burkhardt, E.; Adham, I.; M; Hobohm, U.; Murphy, D.; Sander, C.; Engel, W.
Hum. Genet. 94, 91-94, 1994
A; Title: A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).
A; Reference number: 154278; MUID:94307715
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A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                      64.0%; Score 96; DB 1; Length 44; 80.0%; Pred. No. 1.9e-07; 2: Indels ive 2; Mismatches 2; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relaxin - little skate (fragments)
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Best Local Similarity 70.09
Watches 14; Conservative
                                                                                                                                                                                                                                                                                                                                       16; Conservative
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                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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A; Residues: 1-131 <RES>
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A. Accession: A53024
A. Status: preliminary; not compared with conceptual translation
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Gesidues: 1-131 - GBUR>
A. Gross-references: GB: X73636; NID: 9871548; PIDN: CAA52016.1; PID: 9871549
B. Adham, I.M.; Burkhardt, E.; Benahmed, M.; Engel, W.
J. Biol. Chem. 268, 26668-26672, 1993
A. Title: Cloning of a CDNA for a novel insulin-like peptide of the testicular Leydig
A. Title: Cloning of a CDNA for a novel insulin-like peptide of the testicular Leydig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lieydig insulin-like protein precursor - pig
NiAlternate names: Ley I-L
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 303-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C;Accession: A53024; A49687
R;Burkhardt, E.; Adham, I.M.; Brosig, B.; Gastmann, A.; Mattel, M.G.; Engel, W. Genomics 20, 13-19, 1994
A;Atile: Structural organization of the porcine and human genes coding for a Leydig of A;Reforence number: A53024; MUID:94292772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   relaxin 2 precursor - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
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A;Residues: 1-166 <EVA>
A;Cross-references: EMBL:227245; NID:g416109; PIDN:CAA81758.1; PID:g416110
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A;Note: sequence extracted from NCBI backbone (NCBIN:140859, NCBIP:140860)
C;Genetics:
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50.7%; Score 76; DB 2; Length 131;
55.0%; Pred. No. 0.0005;
ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Accession: S42786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 RLCGREFIRAVIFTCGGSRW 27
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                                                                                                                                                                                                                                                              8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                32 KLCGHHFVRALVRVCGGPRW 51
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Matches 11; Conservative
                         Query Match 50.79
Best Local Similarity 55.09
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X58369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 19p13.2-p12
A;Introns: 64/1
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A; Residues: 1-131 <ADH>
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Pred. No. 0.0035;

57.1%;

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C:Species: Gorilla (gorilla)
C:Species: Gorilla (gorilla)
C:Decies: Gorilla (gorilla)
C:Decies: Od-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: S42784; S42779
R:Evans, B.B.
Submitted to the EMBL Data Library, November 1993
R:Evans, B.B.
A:Reference number: S42776
A:Accession: S42784
A:Accession: S42784
A:Accession: S42784
A:Accession: S4279
A:Accession: S4279
A:Accession: S4279
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A:Accession: S42779
A:Accession: 
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relaxin 1 precursor - chimpanzee (fragment)
c;Species: Pan troglodytes (chimpanzee)
c;Species: Pan troglodytes (chimpanzee)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S42783
R;Evans, B.B.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
A;Accession: S42783
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Keywords: disulfide bond; hormone
F;1-33/Domain: relaxin chain 2B (fragment) #status predicted <RXB2>
F;34-57/Domain: relaxin chain 2A (fragment) #status predicted <RXA2>
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                                                                             Fil-5/Domain: signal sequence (fragment) #status predicted <SIG>Fi6-166/Product: relaxin 2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;KeFwords: disulfide bond; hormone
F;l-5/Domain: signal sequence (fragment) #status predicted <SIG>
F;6-166/Product: relaxin 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                      Length 166;
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                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                               Query Match 48.0%; Score 72; DB 2;
Best Local Similarity 57.1%; Pred. No. 0.0024;
Matches 12; Conservative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 VRLCGREFIRAVIFTCGGSRW 27
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         relaxin - gorilla (fragments)
A; Gene: rlx2
C; Superfamily: insulin
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A; Residues: 1-166 <EVA>
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C;Genetics:
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Length 166;

DB 2;

47.3%; Score 71;

Query Match

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C;Species: Homo sapiens (man)
C;Date: 03-F90-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C;Date: 03-F90-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999
C;Accession: B05092; A44559
R;Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Treg
EMBO J. 3, 2333-2339, 1984
EMBO J. 3, 2333-2339, 1984
A;Tille: Relaxin gene expression in human ovaries and the predicted structure of a hu
A;Reference number: A05092; MUID:85051298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Cross-references: GB:X00949; NID:g35932; PIDN:CAA25461.1; PID:g35933
B.Hudson, P.: Haley, J.: John, M.; Cronk, M.: Crawford, R.: Haralambidis, J.: Tregear Natures 301, 628-631, 1983
A.Title: Structure of a genomic clone encoding biologically active human relaxin.
A.Reference number: A44559; MuID:83141755
A.Rolecule type: DNA
A.Rolecule type: DNA
A.Rolecule type: DNA
A.Rolecule type: DNA
A.Rolecule type: That acts with estrogen to produce dilation c.comment: Relaxin is an ovarian hormone that acts with estrogen to produce dilation
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C; Date: 03 Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
C; Date: 03 Mar-1994 #sequence_revision 03-Mar-1994 #text_change 08-Dec-2000
C; Accession: A60502 A60502
R; Hudson, P.; John, M.; Crawford, R.; Haralambidis, J.; Scanlon, D.; Gorman, J.; Tree EMBO J. 3, 2333-2339, 1984
A; Title: Relaxin gene expression in human ovaries and the predicted structure of a hua; Reference number: A05092; MUID: 85051298
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R;Stults, J.T.; Bourell, J.H.; Canova-Davis, E.; Ling, V.T.; Laramee, G.R.; Winslow,
Biomed. Environ. Mass Spectrom. 19, 655-664, 1990
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                                                   Gaps
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A.Map position: 9pter-9412

A.Map position: 9pter-9412

A.Map position: 9pter-9412

C.Superfamily: insulin

C.Superfamily: relaxin 1 chain B #status predicted AMAT>

F:26-57,/Domain: relaxin 1 chain B #status predicted AART>

F:162-185,/Domain: relaxin 1 chain A #status predicted ACH>

F:162-185,/Domain: relaxin 1 chain A #status predicted

F:35-172,47-185,171-176/Disulfide bonds: #status predicted
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                                   6; Indels
                                           Mismatches
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                                                                                                                       27
                                                                                                                                                                  13 IKLCGRELVRAQIAICGMSTW 33
                                                                                                                                                                                                                                                                                                                                                                                                                            N:Alternate names: preprorelaxin 1
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                                                                                                                       7 VRLCGREFIRAVIFTCGGSRW
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Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             relaxin 1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-185 <HU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-185 <HUD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
A; Gene: GDB: RLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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Fri Jun 28 11:32:06 2002

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A; Molecule type: protein
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                                                                                                                                                                                                                         A; Cross-references: GDB:119553; QMIM:179740
A; Map position: 9pter-9q12
A; Map position: 9pter-9q12
C; Superfamily: insulin
C; Superfamily: insulin
C; Superfamily: insulin
C; Superfamily: insulin
C; Steywords: ovary; Pyroglutamic acid
C; Reywords: ovary; Pyroglutamic acid (SDF)
C; S5-53, 162-185, Product: relaxin 2 **estatus experimental CAMT>
C; S6-157, Domain: relaxin 2 connecting C peptide **status predicted CCPEP>
C; S6-157, Domain: relaxin 2 chall A; Restatus experimental CACH>
C; S5-172, 47-185, 171-176, Disulfide bonds: **status experimental
C; Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) **status experime
A;Title: Structural characterization by mass spectrometry of native and recombinant humd
A;Reference number: A60982; MUID:91167739
A;Accession: A60982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Species: 13-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Jun-1993
C;Accession: B3-2201
R;Schwabe, C.; Buellesbach, E.E.; Heyn, H.; Yoshioka, M.
J. Biol. _Chem. 264, 940-943, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relaxin - gorilla (fragments)
C;Species: Gorilla gorilla (gorilla)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: S42778; S42777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S42777
A;Molecule type: DNA
A;Residues: 34-57 <EVX>
A;Cross references: EMBL:Z27226; NID:g415948; PIDN:CAA81740.1; PID:g415949
A;Orbe: chain 1A
C;Genetics:
A;Gene: rlx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-33 <EVA>
A; Cross-references: EMBL: Z27227; NID: 9415950; PIDN: CAA01741.1; PID: 9415951
A; Note: chain 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Keywords: disulfide bond; hormone
F;1-33/Domain: relaxin chain 1B (fragment) #status predicted <RXB1>
F;34-57/Domain: relaxin chain 1A (fragment) #status predicted <RXA1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%; Score 71; DB 1; Length 185; 57.1%; Pred. No. 0.0038; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.0%; Score 63; DB 2; Length 57; 52.4%; Pred. No. 0.021; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1993
A;Reference number: $42776
A;Accession: $42778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 VRLCGREFIRAVIFTCGGSRW 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                         A; Molecule type: protein
A; Residues: 25-53;162-185 <STU>
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Matches 11; Conservative
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Cross-references: EMBL:227088; NID:9414780; PIDN:CAA81611.1; PID:9414781
R; Buellesbach, E.E.; Schwabe, C.
Biochem. Biophys. Res. Commun. 196, 311-319, 1993
A; Title: Mouse relaxin: synthesis and biological activity of the first relaxin with a A; Reference number: PNG626; MUID:94030011
A; Reference number: PNG626; MUID:94030011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: proteins with and without 184-Tyr were synthesized, their biological activiti c;Superfamily: insulin c;Keywords: hormone F;23-57,161-185/Product: relaxin #status experimental <MAT>
A;Title: Cetacean relaxin. Isolation and sequence of relaxins from Balaenoptera acuto A;Reference number: A32201; MUID:89093167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Jul-1999
C;Accession: 548082; PC2067; PN0626
R;Evans, B.A.; John, M.; Fowler, K.J.; Summers, R.J.; Cronk, M.; Shine, J.; Tregear, J. Mol. Endocrinol. 10, 15-23, 1993
A;Title: The mouse relaxin gene: nucleotide sequence and expression.
A;Reference number: $48082; MUID:93199663
A;Accession: $48082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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C:Species: Canis lupus familiaris (dog)
C:Date: 27-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Date: 27-Sep-1994 #sequence_revision 26-May-1995
C:Accession: B53879, A53879
R:Stewart, D.R.; Henzel, W.J.; Vandlen, R.
J. Protein Chem. 11, 247-253, 1992
A;Title: Purification and sequence determination of canine relaxin.
A;Reference number: A53879; MUID:93000391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;23-57/Domain: chain B #status experimental <CHB>
F;161-185/Domain: chain A #status experimental <CHA>
F;36-171,48-185,170-175/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                           Length 54;
                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                        40.7%; Score 61; DB 2;
42.9%; Pred. No. 0.039;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      7 VRLCGREFIRAVIFTCGGSRW 27
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Best Local Similarity 52.6'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
'-hac 9; Conserva
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A; Residues: 161-185 <BU2>
                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-54 <SCH>
C;Superfamily: insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-185 < EVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: PN0626
                                                                        A; Accession: B32201
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Liberal relaxin - hamadryas baboon (fragment)
C; Species: Papio hamadryas (hamadryas baboon)
C; Species: Papio hamadryas (hamadryas baboon)
C; Species: Papio hamadryas (hamadryas baboon)
C; Date: 0. 46. Sep-1997 # sequence_revision 07-Nov-1997 # text_change 01-Dec-2000
C; Accession: 156451; 842782
R; Evans, B.B.A.; Fu, P.; Tregear, G.G.W.
J. Mol. Endocrinol. 140, 385-392, 1994
A; Title: Characterization of two relaxin genes in the chimpanzee.
A; Reference number: 156451
A; Reference number: 156451
A; Recession: 156451
A; Recession: 156451
A; Residues: 1-33 < EMBL: 227224; NID:9415994; PIDN:CAA81738.1; PID:9415995
A; Cross-references: EMBL: 227224; NID:9415994; PIDN:CAA81738.1; PID:9415995
A; Coss-references: EMBL: 227224; NID:9415994; PIDN:CAA81738.1; PID:9415995
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: insulin
C; Reywords: hormone
F;1-33/Domain: relaxin chain B (fragment) #status predicted <RXB>
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                      A Experimental Source: placenta
A Note: sequence extracted from NCBI backbone (NCBIP:115401)
A Accession: A53879
A Accession: A53879
A Molecule type: protein
A: Residues: 36-59 <ST2>
A: Experimental source: placenta
A: Residues: 36-59 vsr2>
C: Superfamily: insulin
C: Superfamily: insulin
C: Superfamily: insulin
C: Superfamily: insulin
C: Reywords: hormone
F: 1-35,36-59/Porduct: relaxin #status experimental <MAT>
F: 1-35,00main: chain B #status experimental <CHB>
F: 36-59/Domain: chain A #status experimental <CHA>
F: 9-46,21-59,45-50/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

40.0%; Score 60; DB 2; Length 59;
Best Local Similarity 42.9%; Pred. No. 0.06;
Matches 9; Conservative 5; Mismatches 7; Indels
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38.0%; Score 57; DB 2; Length 33;
Best Local Similarity 52.6%; Pred. No. 0.1;
Matches 10; Conservative 3; Mismatches 6; Indels
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A; Residues: 1-35 <STE>
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Search completed: June 27, 2002, 16:09:27 Job time: 211 sec

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OM protein - protein search, using sw model

June 27, 2002, 16:16:51; Search time 18.68 Seconds (without alignments) 55.965 Million cell updates/sec Run on:

US-09-781-077-2_COPY_26_52 150 1 RAAPYGVRLGGREFIRAVIFTCGGSRW 27

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

.

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ı	DB ID	1 RELX SOUAC	1 RELX_ODOTA	RELX	INLS	1 INL3_HUMAN	INE	1 INL3_BOVIN	1 INL5_MOUSE	- 1	1 REL1_PANTR	1 REL1_HUMAN	REL2	1 INL3_RAT	1 INL3_CALJA	1 INL3_MOUSE	1 RELX_BALAC	1 RELX_MOUSE	1 RELX_MACMU	1 RELX_BALED	1 RELX_MESAU	1 RELX_PIG				1 INL6_RAT	RELX	ILB5_	RELX	1 SUHW_DROAN		1 ZFG1_HUMAN	1 ZFG1_MOUSE	1 ILB1_CAEEL
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RESULT 2 RELX_ODOTA

	PRT; 54 AA. Hence update) teation update) traniata; Vertebrata; Chondrichthyes; traniata; Vertebrata; Chondrichthyes; idei; Squalidae; Squalus. 7; the sequence of relaxin from spiny 86). telaxin IN AN OVIPAROUS SPECIES IS NOT ted. INSULIN/IGF/RELAXIN FAMILY. E_relaxin. F_relaxin. TERCHAIN. TERCHAIN. TERCHAIN. TERCHAIN. TERCHAIN.	DB 1; Length 54; .3e-11; as 0; Indels 0; Gaps 0;
INS_HYDCO INS_CALMI ILB3_CAEMI ILB3_CAEMI INL6_HUMAN RELX_DASSA RELX_DASSA RELX_DASSA RUSM_HIPAM NUSM_HIPAM NUSM_DASNO NUSM_DIDMA NUSM_DIDMA NUSM_MACRO	ALLUNMENTS ALLUNMENTS (*) Created) (*) Last sequence update) (*) Last sequence update) (*) Last annotation and the sequence of uthias) (*) Last annotation update) (*) Last annotati	Score 116; D Pred. No. 6.3 3; Mismatches 27
	ARD; PR , Created) , Last seque , Last seque , Last annot piny dogfish Chordata; Cr lea; Squaloi an L.K., Sch tion, and th nthias).", 135-341(198 NCTION: Secret IMER OF A B IMER OF A B IMI, 1. SULIN, 1. SULIN; 1. SULIN; 1. SULIN; 1. SULIN; 1. SULIN; 1. 30 11 PREL 54 11 INTI	m (4 m
59 103 213 201 201 598 602 602	STANDARD; PRT; (Rel. 12, Created) (Rel. 28, Last sequenc. (Rel. 40, Last annotatenthias (Spiny dogfish). Metazoa; Chordata; Cranhi; Squalea; Squaloide (1797; Purification, and the qualus acanthias)."; Schwan L.K., Schwan, 161:335-341(1986) NN: THE FUNCTION OF RELAWING. THE FUNCTION OF RELAWING. THE FUNCTION: Secreted (1772; BELONGS TO THE INS. (1874) A.26463. (26 KLX. (26 KLX. (27 STANDIN) 1. (28 STANDIN) 1. (28 STANDIN) 1. (29 STANDIN) 1. (20 STANDIN) 1. (21 STANDIN) 1. (21 STANDIN) 1. (21 STANDIN) 1. (22 STANDIN) 1. (23 STANDIN) 1. (24 STANDIN) 1. (25 STANDIN) 1. (26 STANDIN) 1. (27 STANDIN) 1. (27 STANDIN) 1. (28 STANDIN) 1. (77.39 86.49 vative TFTCGS1
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4444444444 000000000000000000000000000	SSOUAC 31-1985 11-1985 11-2001	/ Match Local Simines 19; G GVRLCGR
88888888888888888888888888888888888888	RESULT 1 RELX_SQUAGO ID RELX_SQUAGO DT 01-FE DT	Query M Best Lo Matches Qy 6

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NCBI_TaxID=9606;
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                                                                                                                                     Gowan L.K., Reinig J.W., Schwabe C., Bedarkar S., Blundell T.L., "On the primary and territy structure of relaxin from the sand tiger shark (Odontaspis taurus)."; FEBS Lett. 129:80-82(1981).
                                                         Odontaspis taurus (Sand tiger shark) (Eugomphodus taurus).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Odontaspididae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
NCBI_TaxID=7782;
                                                                                                                                                                                                     MEDLINE-87054035; PubMed-3780747;
Bullesbach E.E., Gowan L.K., Schwabe C., Steinetz B.G., O'Byrne E.,
                                                                                                                                                                                                                            "Isolation, purification, and the sequence of relaxin from spiny dogfish (Squalus acanthias).";
Eur. J. Bacchen. 161:335-341(1986).
-!- SUBGNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%; Score 96; DB 1; Length 44; 80.0%; Pred. No. 5.2e-08; 1:ve 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
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6122F6604C660607 CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                   21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            RELAXIN B CHAIN.
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  44 AA.
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Paran; PR00049; Insulin; 1.
SMART; SW00078; IIGF; 1.
PROSITE; PS00262; INSULIN; 1.
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  PRT;
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MEDLINE=87156758; PubMed=3827922;
                                                                                                                                 MEDLINE-82004703; PubMed-7274472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QLCGRGFIRAIIFACGGSRW 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                               4730 MW;
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                        Insulin family; Hormone.
  STANDARD;
                                                                                                                                                                                                                                                                                                       PIR; A01616; RXRKOT.
                                                   Relaxin (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                44 AA;
                                                                                                   NCBI_TaxID=30501;
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  RELX_ODOTA
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99389725; PubMed=10458910;
Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
Bullesbach E.E., Schwabe C., Callard I.P.;
"Relaxin from an oviparous species, the skate (Raja erinacea).";
Biochem. Biophys. Res. Commun. 143:273-280(1987).
-:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Insulin-like peptide INSL5 precursor (Insulin-like peptide 5).
                                                                                                                                                -i- SUBCELLULAR LOCATION: Secreted.
-i- SINILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
PIR; A29543; A29543.
HSSP, P04090; GRLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.0%; Score 87; DB 1; Length 64; 70.0%; Pred. No. 1.7e-06; Live 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7AC62B8BA81F49D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELAXIN A CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                           RELAXIN B CHAIN
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SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                   InterPro; IPR000739; Insulin_IGF_relaxin. Pfam; PF00049; Insulin; 1. SMART; SM00078; IIGF; 1. PROSITE; PS00262; INSULIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7499 MW;
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Best Local Similarity 70.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          Insulin family; Hormone.
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                                                                                                                         DISULFIDE BONDS
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Ilu S.,
Attix C., Andrelse T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
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MEDLINE-4307715; PubMed-8034302;
MEDLINE-4307715; PubMed-8034302;
MINTAGET E., Adham I.M., Hobohm U., Murphy D., Sander C., Engel W.;
"A human cDNA coding for the Leydig insulin-like peptide (Ley I-L).";
Hum. Genet. 94:91-94(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                           POTENTIAL.
INSULIN-LIKE PEPTIDE INSLS B CHAIN (POTENTIAL).
                                                                                                                                                                          INSULIN-LIKE PEPTIDE INSL5 A CHAIN
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SUCCELLAR LOCATION: SECRETEG.
SUBCELLULAR LOCATION: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTUNTAL LEYDIG CELLS. FOUND AS WELL IN THE CORPUS LUTEUM, TROPHOBLAST, FETAL MEMBRANES AND BREAST.
                                                                                                                                               CONNECTING PEPTIDE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                    54.7%; Score 82; DB 1; Length 135; 66.7%; Pred. No. 1.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.9e-05;
; Mismatches 5; Indels
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INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
98FFCB20E9C4BC1F CRC64;
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                                Hormone; Signal.
                                                                                                                                                                                                                                                                                                                 15318 MW;
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PS00262; INSULIN; 1.
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135 AA;
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Best Local Similarity
Matches 14; Conserv
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                          Insulin family;
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115
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  PROSITE;
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adham I.M., Burkhardt E., Benahmed M., Engel W.; "Cloning of a cDNA for a novel insulin-like peptide of the testicular Leydig cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                    C PEPTIDE (POTENTIAL).
LEXDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Bukaryota; Motazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                       LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94292172; PubMed-8020942;
Burkhardt E., Adham I.M., Brosig B., Gastmann A., Mattei M.-G.,
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-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.7%; Score 76; DB 1; Length 131; 55.0%; Pred. No. 0.00015;
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C5799D610424C136 CRC64;
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                                                                                                                                                                                                          InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                    .1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
MEDLINE=94075362; PubMed=8253799;
                                                                                                                                                                                                                                                                       Insulin family; Hormone; Signal
                                                                                                                                                               EMBL; X73637; CAA5201/.1; ALL.
EMBL; AC005952; AAC72277.1; -.
                                                                                                                                                                                                                                                          PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               14472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KLCGHHFVRALVRVCGGPRW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                    EMBL; S72482; AAB31371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                     55
104
131
116
129
120
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                              MIM; 146738; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSL3 OR RLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INL3_PIG
P51461;
                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Engel W.;
                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                    CHAIN
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INL3_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
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us-09-781-077-2_copy_26_52.rsp

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                                                                                                               Insulin family; Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
                                              EMBL; AF094580; AAC63380.1; -.
                                                                                                                                                                                                                       14378 MW;
                                                                                                  PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                        32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                         INL5_MOUSE
Q9WUG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hsu S.Y.;
                                                                                                                                                                                DISULFID
                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                         PROPEP
                                                                                                                               SIGNAL
                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                            INL5_MOUSE
                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED unstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is non oway modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      077801;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide precursor (Ley-I-L) (Relaxin-like factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bathgate R.A.D., Balvers M., Hunt N., Ivell R.; "Relaxin-like factor gene is highly expressed in the bovine ovary of the cycle and pregnancy: sequence and messenger ribonucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULEDIDE BONDS (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED EXCLISIVELY IN LEYDIG CELLS.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                            POTENTIAL.
LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                         ó
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PRENATAL AND POSTNATAL LEYDIG CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol, Reprod. 55:1452-1457(1996).
                                                                                                                                                                                                                                                                                                                                                                                             Score 75; DB 1; Length 131;
Pred. No. 0.00021;
; Mismatches 5; Indels
                                     -! SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                        8AB718870859EF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AA
                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97107158; PubMed=8949906;
                                                                                                                                                                                                                                                    Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                      25 56 LE
58 103 C
106 131 LE
34 116 IN
46 129 IN
115 120 BY
                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                     EMBL; X73636; CAA52016.1; -.
                                                                                                                                                                                                                         SMART; SM00078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 KLCGHHFVRALVRLCGGPRW 51
                                                                                                                                                                                   CAA48449.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Ce<sup>°</sup>
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Testis;
                                                                                                                                                                                   EMBL; X68369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSL3 OR RLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INL3_BOVIN
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INL3_BOVIN
                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conklin D., Lofton-Day C.E., Haldeman B.A., Ching A., Whitmore T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of two novel mammalian paralogs of relaxin/insulin family proteins and their expression in testis and kidney."; Mol. Endocrinol. 13:2163-2174(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                    C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                          LEYDIG INSULIN-LIKE PEPTIDE B CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MXY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1nsulin-like peptide INSL5 precursor (Insulin-like peptide 5)
(Relaxin/insulin-like protein) (Relaxin/insulin-like factor 2).
INSL5 OR ZINS3 OR RIF2 OR RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 75; DB 1; Length 132; 55.0%; Pred. No. 0.00021; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A5585500C7F2241D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                   InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB; TISSUE=Ovary;
MEDLINE=20065648; PubMed=10598589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Colon;
MEDLINE-99389725; PubMed=10458910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                   (POTENTIAL).
CONNECTING PEPTIDE (POTENTIAL).
INSULIN-LIKE PEPTIDE INSL5 A CHAIN
                                                                                                                                                                                                                         INSULIN-LIKE PROTEIN INSL5 B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evans B.A., Fu P., Tregear G.W.; "Characterization of two relaxin genes in the chimpanzee."; J. Endocrinol. 140:385-392(1994).
                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 75; DB 1; Length 135; 52.4%; Pred. No. 0.00022; tive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      05FF9A0F613DBF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                          InterPro; IPR000739; Insulin_IGF_relaxin.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                           POTENTIAL.
                                                                                              EMBL; AF076971; AAD48089:1; -:
EMBL; AF054842; AAF09093:1; ALT_INIT.
EMBL; AF054843; AAF09094:1; -:
EMBL; BC010958; AAH10968:1; -:
MGD; MGI:1346085; INS15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prorelaxin H2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94238260; PubMed=8182365;
                                                                                                                                                                                               Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILL2_PANTR STANDARD; P. P51455; P79267; Ol-OCT-1996 (Rel. 34, Last seque 16-OCT-2001 (Rel. 40, Last annotation)
                                                                                   EMBL; AF133817; AAD29687.1; -.
                                                                                                                                                                                    PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                       15524 MW:
                                                                                                                                                                                                                                                                                                                                                                                                        7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                      26 VKLCGLDYVRTVIYICASSRW 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                 Ins15
                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        121
135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS
                                                                                                                                                                                                                                              49
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Placenta;
                                                                                                                                                                                                                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNL2 OR RLX2
                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL
                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
REL2_PANTR
                                                                                                                                                                                                                                                                                                                                                                              Matches
Q
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-!- SUBCELLULAR LOCATION: Secreted

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVANS B.A., FU P., Tregear G.W.;
"Characterization of two relaxin genes in the chimpanzee.";
"Characterization of two relaxin genes in the chimpanzee.";
"Characterization of two relaxin genes in the chimpanzee.";
-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN ANY MAMALS. MAY BE INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PREGNACY, PROMOTING GROWTH OF PUBLIC LIGAMENTS AND RIPENING OF THE CREVIX.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVPSFINKDTETINMMSEFVANLPOELKLTLS -> DFIO
TVSLGISPDGGKALRTGSCFTREFLGALS (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
               produced by alternative splicing.
--- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY AND IN THE PLACENTA.
---- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal; Polymorphism;
Alternative splicing.
   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MÍSSING (IN ISOFORM 2). *
KSTWS -> MSTLG (IN SOME ALLELES).
220851E3134CEBDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

RELAXIN B CHAIN (PROBABLE).

CONNECTING PEPTIDE (PROBABLE)

RELAXIN A CHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 1; I
Pred. No. 0.00075;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-077-1996 (Rel. 34, Created)
01-077-1996 (Rel. 34, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prorelaxin Hi precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94238260; PubMed-8182365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 K
18760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 IKLCGRELVRAQIAICGKSTW 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                   EMBL; 227245; CAA81758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.18;
                                                                                                                                                                                                                                                  EMBL; S83209; AAD14430.1;
HSSP; P04090; 6RLX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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1138
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30
166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
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P51454;
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SEQUENCE
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SIGNAL
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PROPEP
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REL1_PANTR
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-83141755; Pubmed=6298628;
Hudson P., Haley J., John M., Cronk M., Crawford R., Haralambidis J.,
Tregear G., Shine J., Niall H.;
Structure of a genomic clone encoding biologically active human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
"Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of CDNA clones.";
EMBO J. 3:2333-2339(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                     -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY
BUT NOT IN THE PLACENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarfilni; Hominidae; Homo.
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CONNECTING PEPTIDE (PROBABLE).
RELAXIN A CHAIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3%; Score 71; DB 1; Length 166; 57.1%; Pred. No. 0.0011; tive 3; Mismatches 6; Indels
                                                                              SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7F469B1FB9259F4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELL_HUMAN STANDARD; PRT; 185 AA. P04808; 099936; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Prorelaxin H1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                                                                                                                                        InterPro; IPR000739; Insulin_IGF_relaxin.
Pfam: PF00049; Insulin; 1.
SMART; SW00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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MEDLINE=85051298; PubMed=6548702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18730 MW;
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                                                                                                                                                                                                                                                                                           EMBL; 227225; CAA81739.1; -. HSSP; P04090; 6RLX.
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Matches 12; Conservative
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SIGNAL
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CONNECTING PEPTIDE (PROBABLE).
RELAXIN A CHAIN (PROBABLE).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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ALSKLYHPSSTKIQKL (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                       TISSUE-PROSTAGE;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-96128899; PubMed=8735594;
MEDLINE-961289; MEDLINE Relaxin mRNA species.";
MOI. Cell. Endocrinol. 118:85-94(1996).
IN SEADINI IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN NANY MAMMALS. MAY BE INCOLOR IN REMORDEING OF CONNECTIVE TISSUES DURING PREGNANCY, PROMOTING GROWTH OF PUBLIC LIGAMENTS AND RIPENING OF THE CERVIX.

-1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Secreted.
-i- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are produced by alternative splicing.
-i- TISSUE SPECIFICITY: Prostate. Not expressed in placenta, decidua
                                                                                                                                                                          PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i - SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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/FTId=VAR_011962.
B318628ABFEC7142 CRC64;
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Insulin family; Hormone; Multigene family; Signal;
Alternative splicing; Polymorphism.
SIGNAL 1 22 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000739; Insulin_IGF_relaxin.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00276; INSULINA.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X00949; CAA25461.1; EMBL; V00578; CAA23839.1; EMBL; V00577; CAA23838.1; EMBL; A06926; CAA00603.1; EMBL; A07364; CAA00599.1; EMBL; A17329; CAA01325.1; EMBL; A17329; CAA01325.1; EMBL; BC005956; AAH05956.1; -
                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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HSSP; P04090; 6RLX.
MIM; 179730; -.
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28
                                                                               TISSUE-Prostate;
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163
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                                                                                                     Strausberg R.;
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MEDLINE-85051298; PubMed-6548702;
Hudson P., John M., Crawford R., Haralambidis J., Scanlon D.,
Gorman J., Tregear G., Shine J., Niall H.;
"Relaxin gene expression in human ovaries and the predicted structure
of a human preprorelaxin by analysis of cDNA clones.";
EMBO J. 3:2333-2339(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "X-ray structure of human relaxin at 1.5 A. Comparison to insulin and implications for receptor binding determinants.";
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91250367; PubMed-2040595;
Buellesbach E.E., Schwabe C.;
"Total synthesis of human relaxin and human relaxin derivatives by
solid-phase peptide synthesis and site-directed chain combination.";
J. Biol. Chem. 266:10754-10761(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winslow J.W., Shih A., Bourell J.H., Weiss G., Reed B., Stults J.T., Goldsmith L.T., "Human seminal relaxin is a product of the same gene as human luteal
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gunnersen J.M., Fu P., Roche P.J., Tregear G.W.;
"Expression of human relaxin genes: characterization of a novel alternatively-spliced human relaxin mRNA species.";
Mol. Cell. Endocrinol. 118:85-94(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winslow J.W., Griffin P.R., Rinderknecht E., Vandlen R.L.; "Structural characterization by mass spectrometry of native and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92015205; PubMed-1656049;
Eigenbrot C., Randal M., Quan C., Burnier J., O'Connell L.,
Rinderknecht E., Kossiakoff A.A.;
47.3%; Score 71; DB 1; Length 185; 57.1%; Pred. No. 0.0012; 1ive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sehra H.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blomed. Environ. Mass Spectrom. 19:655-664(1990).
                                                                                                                                                                                REL2_HUMAN STANDARD; PRT; 185 AA. P04090; Q9UCX3; Q99936; 01-NOV-1986 (Rel. 03, Lose tequence update) 01-NAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96328899; PubMed=8735594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endocrinology 130:2660-2668(1992).
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                                                                                    7 VRLCGREFIRAVIFTCGGSRW 27
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                               12; Conservative
                                                                                                                                                                                                                                                                      Prorelaxin H2 precursor.
                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                 Best Local Similarity
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Query Match
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                             Matches
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LOOHVP -> GDFIQTVSLGISPDGGKALRTGSCFTREFLG
ALSKLCHPSSTKIQKP (IN ISOFORM 2).
                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in the ovary during pregnancy. Also expressed in placenta, decidua and prostate.
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
J. Mol. Biol. 221:15-21(1991).

-!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE INVOLVED IN REMODELING OF CONNECTIVE TISSUES DURING PRECNANCY, PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.
-!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Insulin family; Hormone; Multigene family; Signal; 3D-structure;
Alternative splicing.
SIGNAL
25 54 RELAXIN B CHAIN.
PROPEP 56 157 CONNECTING PEPTIDE.
CHAIN 162 185 PYRROLIDONE CARBOXYLIC ACID.
DISULFID 35 172 INTERCHAIN.
DISULEID 47 185 INTERCHAIN.
AVARSPLIC 71 117 EIVPSFINKDTETINMASEFVANLEOGLKITLSEMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score /1; ____Pred, No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21042 MW; AC73DBDE2090091B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                    EMBL; X00948; CAA25460.1; -. BMBL; AL13798; CAC04177.1; -. EMBL; AL135786; CAC04176.1; -. EMBL; S83200; AAD14429.1; -. EMBL; A06925; CAA01324.1; -. EMBL; A06925; CAA00602.1; -. PIR; A06922; A60982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.10,
'-has 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00049; Insulin; 1.
SMART; SM00078; IIGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 IKLCGRELVRAQIAICGMSTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 6RLX; 31-OCT-93.
MIM; 179740; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INL3_RAT
Q9WUK0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ID INL3_
AC Q9WUF
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STRAIN=129/SVJ;
Zimmermann S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INL3_CALJA STANDARD; PRT; 131 AA.
097937; 097938;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
18-0CT-2001 (Relaxin-like factor).
                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Callithix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                 DISULFIDE BONDS (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.
--- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                          Spiess A.-N., Pusch W., Ivell R.; "Cloning and sequence of the rat relaxin-like factor and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.7%; Score 70; DB 1; Length 105; 50.0%; Pred. No. 0.00096;
 16-OCT-2001 (Rel. 40, Created)
LeCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Leydig insulin-like peptide (Ley-I-L) (Relaxin-like factor)
                                                                                                                                                                                               Elbmitted (MAR-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
903716A8FBEB13EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF139918; AAD33663.1; -.
InterPro; IPR000739; Insulin_IGF_relaxin.
Pram; PF00049; Insulin; 1.
SMART; SW00078; I1GF; 1.
PROSITE; PS00262; INSULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11674 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          # KLCGHHLVRALVRVCGGPRW 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 RLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.0 es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insulin family; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77
105
90
103
                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
18
89
105 /
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9483;
                                                                                                           NCBI_TaxID=10116;
                                                               INSL3 OR RLF.
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                                                                                                                                                                                        promotor."
                                                   Fragment)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INL3_CALJA
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1NL3_MOUSE 37744;
01-NOV-1997 (Rel. 35, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
10-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2002 (Rel. 41, Last annotation update)
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=99115234; PubMed=9916013;
Zarreh-Hoshyari-Khah M., Einspanier A., Ivell R.;
"Differential splicing and expression of the relaxin-like factor gene in reproductive tissues of the marmoset monkey (Callithrix Jacchus).";
Biol. Reprod. 60:445-453(1999).
-i- FUNCTION: COULD PLAY A ROLE IN TESTICULAR FUNCTION AND
                                                                                                                                                                                                                                                                                                                                                                                                  SHORT/TRUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                  -:- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULRIDE BONDS (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Secreted.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELLQWLERRH -> ESHSAAQDGGQ (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SHORT ISOFORM). 685743CAEECF8731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00049; Insulin; 1.
SMART; SM00078; ILGF; 1.
PROSITE; PS0026: INSULIN; 1.
Insulin family; Hormone; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000739; Insulin_IGF_relaxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I SOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ011961; CAA09888.1; -.
EMBL; AJ011962; CAA09888.1; JOINED.
EMBL; AJ011961; CAA09889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 KLCGHHFVRALVRVCGGPLW 51
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131
117
130
121
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                                                                                                                                                                                                                                                    SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 AA;
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P01315; 1ZEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                       STRAIN-129/SVJ;

XX MEDLINE-98088907; PubMed-9428631;

XA KOSKIMISE P., Spiess A.N., Lahti P., Huhtaniemi I., Ivell R.;

AA KOSKIMISE P., Spiess A.N., Lahti P., Huhtaniemi I., Ivell R.;

RT The mouse relaxin-like factor gene and its promoter are located

RT within the 3' region of the JAK3 genomic sequence.";

RL FEBS Lett, 419:186-190(1997).

FEBS Lett, 419:186-190(1997).

CC -1 SUBKATOGENESIS.

CC -1 SUBKATOGENESIS.

CC -1 SUBKATI BERRODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO

DISULFIDE BONDS (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: Secreted.

CC -1 SUBCELLULAR LOCATION: Secreted.

CC -1 SUBCELLULAR LOCATION: SECRETEGO.

CC -1 SUBCELLULAR LOCATION: SECRETEGO.

CC -1 SUBCELLULAR LOCATION: SECRETEGO.

CC -1 SUBLIBARITY: EXPRESSED EXCLUSIVELY IN LEYDIG CELLS.

CC -1 SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                           Pusch W., Balvers M., Ivell R.; "Molecular cloning and expression of the relaxin-like factor from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEYDIG INSULIN-LIKE PEPTIDE B CHAIN.
C PEPTIDE (POTENTIAL).
LEYDIG INSULIN-LIKE PEPTIDE A CHAIN.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
P -> T (IN REF. 1).
VETRO -> CGDPG (IN REF. 1).
A -> S (IN REF. 1).
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A -> S (IN REF. 1).
QRQRR -> HARG (IN REF. 1)..
10783AB4896CF103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S82815; AAB39365.1; --
EMBL; AF136524; AAD4585.1; --
MGD; MG108427; Ins13
InterPro; IPR000739; Insulin_IGF_relaxin.
Prant; PF00049; Insulin; 1.
PROSITE; PS00262; INSULIN; 1.
Insulin family; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                             Endocrinology 137:3009-3013(1996).
                                                     TISSUE=Testis;
MEDLINE=96366811; PubMed=8770925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X95603; CAA64861.1; -.
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                              mouse testis,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
DISULFID
DISULFID
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0; Gaps

Ouery Match
Best Local Similarity 45.0%; Pred. No. 0.0044;
Matches 9; Conservative 4; Mismatches 7; Indels

Search completed: June 27, 2002, 16:16:52 Job time: 486 sec

8 RLCGREFIRAVIFTCGGSRW 27 :||| :| :| || || 27 KLCGHHLVRTLVRVCGGPRW 46

QY Db

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2002, 16:16:28 ; Search time 58.57 Seconds (Without alignments) 79.748 Million cell updates/sec Run on:

US-09-781-077-2_COPY_26_52 150 Perfect score:

1 RAAPYGVRLCGREFIRAVIFTCGGSRW 27 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_archea:*
sp_bacteria:*
sp_fung:*
sp_fung:*
sp_human:*
sp_mammal:*
sp_mammal:*
sp_mhc:* sp_virus:* sp_vertebrate:* sp_unclassified:* 10: \$P_Glant:*
11: \$P_rodent:*
12: \$P_virus:*
13: \$P_vertebrate:*
14: \$P_unclassified:
15: \$P_acteriap:*
17: \$P_archeap:* sp_phage:* sp_plant:* sp_rodent:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description			Q9uph6 homo sapien	O9nOt8 dama dama (_	•		-	Q28429 gorilla gor		Odmyka folia ofluo	COLOR LELLS SILVE	220/00 papto namad	. Camerus dro	09trq5 sus scrofa	028782 Opdon C87820		Cazaya irankia sp.	•		
	Ω		Control	90540	SANCE	9GK47	528431	820N60	00.400	67407	29NOF2	9MYK8	28788	OFUNDO	1000	291.KG5	28782	7925V5	100	794555	9VFK9	
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Q52064 pantoea agg Q28780 papio hamad Q99kt9 mus musculu O57687 taenopygia	gallus gallus lomo sap nus mus	shige esche 9 arab 4 pseu 3 mus	1664644	Q9mkj0 gorilla gor Q959c5 galaxias fa Q959b1 galaxias vu Q9ta02 lampetra fl Q47815 geomys pers Q9g383 echinops te Q9blr0 homo sapien
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17 18 19 20 21	22 22 22 25 26	27 28 30 31 31	3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	330 444 444 45

ALIGNMENTS

			ate)	pdate)				brata; Euteleostomi:								mber of the	frog Rana esculenta "	Endocrinology 142:3231-3238(2001).	RITY).	-!- SIMILARITY: BELONGS TO THE INSULIN/IGE/RELAXIN FAMILY.							34 CRC64;	3; Length 155;	
	I; 155 AA.	red)	Last sequence update)	Last annotation update)				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;						De Rienzo G., Aniello F., Branno M., Minucci S.	"Isolation and characterization of a novel member of the	estis of the		ID (BY SIMILA	SULIN/IGF/RE		relaxin.				WN 1	517ADA5385026E34	Score 104; DB 13;	(
	RY; PRT;		16,	. 19,			e frod).	hordata; Cra	Anura; Neoba					MEDLINE=21309007; PubMed=11416046;	F., Branno	terization	from the t	1-3238(2001)	ION: SECRETE	3S TO THE IN	108.1;	InterPro; IPR000739; Insulin_IGF_relaxin.	W Mtase.	1, 1,		PROSITE; PS00092; N6 MTASE; UNKNOWN 1	17470 MW; 51	69.3%; Scor	
	PRELIMINARY;	1 (TremBLrel	(TrEMBLrel.	(TremBLrel	RELAXIN-LIKE PROTEIN.		Rana esculenta (Edible frog).	Metazoa; C	Batrachia;	-8401;		ROM N.A.	is:	109007; Publ	i., Aniello	and charact	ulin family	ogy 142:323	ULAR LOCAT	RITY: BELONG	EMBL; AJ298874; CAC16108.1;	:PR000739;]	PR002052; 1	Pfam; PF00049; Insulin; 1.	SMART; SM00078; IlGF; 1.	00092; N6 N	155 AA; $\overline{17}$		
LT 1 P8	Q9DEP8 Q9DEP8;	01-MAR-2001	01-MAR-2001	01-DEC-2001	RELAXIN-LIF	INSL3.	Rana escule	Eukaryota;	Amphibia; E	NCBI_TaxID=8401;	[1]	SEQUENCE FROM N.A.	TISSUE=TESTIS;	MEDLINE=213	De Rienzo G	"Isolation	relaxin/ins	Endocrinolc	- i - SUBCELI	-!- SIMILAR	EMBL; AJ298	InterPro; I	InterPro; I	Pfam; PF000	SMART; SM00	PROSITE; PS	SEQUENCE	Query Match	
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32 KLCGHHFVRALVRLCGGPRW 51

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Hombach-Klonisch S., Kauffold J., Rautenberg T., Steger K., Tetens F.,
Fischer B., Klonisch T.;
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Burkhart-Schultz K., Gordon L., Dias J., Sakaldasis G., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Danganan L.,
Erler A., Christensen M., Georgescu A., Avila J., Attix C.,
Andreise T., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Sanders C.,
Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
Sequence analysis of a 5.7 Mb region in 19913.1.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
BMBL, AC007201; AAD22740.1; -.
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                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Relaxin-like factor (RLF) mRNA expression in the fallow deer."; Mol. Cell. Endocrinol. 159:147-158(2000).
-! SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 75; DB 6; Length 131; Best Local Similarity 55.0%; Pred. No. 0.00075; Matches 11; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 50.7%; Score 76; DB 4; Length 65; Best Local Similarity 55.0%; Pred. No. 0.00026; Matches 11; Conservative 4; Mismatches 5; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RELAXIN-LIKE PROTEIN.
                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                PRT;
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PROSITE; PS00262; INSULIN; 1.
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                                       PRELIMINARY;
                                                                                                                                     INL3_HUMAN (FRAGMENT).
                                                                                                                                                          Homo sapiens (Human)
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SEQUENCE
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                                                                                                                              Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                                                                                                                              MOI. BIOI. EVOI. 0:0-0(2001).
-:- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
EMBL; AF317624; AAG42317.1; -.
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SMART; SM0078; IlGF; 1.
PROSITE; PS00262; INSULIN; 1.
SEQUENCE 131 AA; 14414 MW; F18AFA9ACFC85943 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:0-0(1993).
BEBL: Z27237; CAA81751.1; -.
HSSP; P04090; 6RLX.
                              PRT; 131 AA
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Best Local Similarity 55.09
Matches 11; Conservative
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                                                                                                                   RELAXIN-LIKE PROTEIN.
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Best Local Similarity
Matches 12; Conserv
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Membach Klonisch S., Tetens F., Kauffold J., Steger K., Fischer B.,
                                                                                                                Capra hirous (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                "Molecular cloning and localization of caprine relaxin-like factor (RLF) mRNA within the goat testis.", Mol. Reprod. Dev. 53:135-141(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla;
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                                                                                                                                                                                                                                                                                                                                                                   Hombach Klonisch S., Klonisch T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-: SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-: SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.

EMBL; AF233686; AAF60301.1; -

InterPro: IRR000739; Insulin_IGF_relaxin.

Fram; PF00049; Insulin; 1.

SWART; SM00078; IIGF; 1.

PROSITE; PS00262; INSULIN; 1.

SEQUENCE 131 AA; 14160 MW; 2A82EB59EA07313A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                      01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Evans B.B.A., Fu P., Tregear G.G.W.;
Evans B.B.A., Fu P., Tregear G.G.W.;
Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:0-0(1993).
EMBL; 22727; CAA81741.1;
HSSP; P04090; GRLX.
                                  131 AA.
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                                                                                                                                                               Bovidae; Caprinae; Capra.
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                             PRELIMINARY;
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SEQUENCE
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RESULT
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                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                      Hasegawa T.;
"Nucleotide sequence of equine Leydig cell-specific insulin-like
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                            7; Indels
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Pred. No. 0.056;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                        peptide.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033169; BAA97580.1;
                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LEYDIG CELL-SPECIFIC INSULIN-LIKE PEPTIDE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                         73 AA; 8125 MW; B9DCBA6D0D72C8BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                          73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 AA.
                            Mismatches
                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=THOROUGHBRED; TISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                 7 VRLCGREFIRAVIFTCGGSRW 27
                                                                 8 IKLCGCELVRAQIAICGMSTW 28
                                                                                                                                                                                                                                                                                                                                                                                                                                            40.78;
Query Match
Best Local Similarity 52.4%
Matches 11; Conservative
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Best Local Similarity 52.97
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 GREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |:||:: ||| ||
1 GHHFVRALVRVCGGPRW 17
                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                              Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9685;
                                                                                                                                                                           01-OCT-2000
                                                                                                                                                                                                                                                                                                                   Hasegawa T.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                       Q9N0F2
Q9N0F2;
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                                                                                                               RESULT
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Q9MYK8
                                                                                                                            Q9NOF2
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Gaps

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Kohsaka T., Takahara H., Sugawara K., Tagami S.;
"Endogenous heterogeneity of relaxin and sequence of the major form in
                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                               Query Match
38.0%; Score 57; DB 6; Length 199;
Best Local Similarity 47.6%; Pred. No. 0.65;
Matches 10; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 29
                         199 AA; 22386 MW; F69BBD7E4F4A8089 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. Hoppe-Seyler 374:203-210(1993).
HSSP; P01348; 1RLX.
SEQUENCE 29 AA; 3293 MW; 661A9F5DDDE5DB10 CRC64;
                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RELAXIN R-III B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.7%; Score 55; DB 6
38.1%; Pred. No. 0.18;
                                                                                                                                                                                                                             29 AA.
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4; Mismatches
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Pred. No. (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VRLCGREFIRAVIFTCGGSRW 27
          PROSITE; PS00262; INSULIN; 1. SEQUENCE 199 AA; 22386 MW;
                                                                                                                                                       32 VKACGRELVRLWIEICGSVSW 52
                                                                                                                            7 VRLCGREFIRAVIFTCGGSRW 27
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47.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                PRELIMINARY;
SMART; SM00078; IlGF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 pregnant sow ovaries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity.
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                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameluse; Camelus
                                                                                                                                                                                                                                                                                                                                                 Eukryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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"Characterization of two relaxin genes in the chimpanzee.";
". Mol. Endocrinol. 140:385-392(1994).
EMBL; 227224; CA881738.1; -.
HSSP; P04090; GRLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20191540; Pubmed-10727251;
Hombach-Klonisch S., Abd-Elnaeim M., Skidmore J.A., Leiser
Fischer B., Klonisch T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ruminant relaxin in the pregnant one-humped camel.";
Bloi. Reprod. 62:189 646(2000).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
BRISP; P01348; ARF67741.1;
-- HSSP; P01348; IRELX.
InterPro; IPRO00739; Insulin_IGF_relaxin.
                                                                     Score 61; DB 6; Length 180; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57; DB 6; Length 33;
Pred. No. 0.1;
3; Mismatches 6; Indels
                                                                                                     8; Indels
                PROSITE; PS00262; INSULIN; 1.
SEQUENCE 180 AA; 20360 MW; 4C2CF371C698AF9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 33 AA; 3618 MW; DD8498A0353F9281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                    33 AA.
                                                                                                     3; Mismatches
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01-NOV-1996 (TrEMBLREL: 01, Last sequ
01-DEC-2001 (TrEMBLREL: 19, Last anno
                                                                                                                                                                                                                                                                                                                                     Papio hamadryas (Hamadryas baboon).
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                                                                                                                                                  30 LKACGREFVRLOIRICGSLSW 50
                                                                                                                                  7 VRLCGREFIRAVIFTCGGSRW 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.0%;
Best Local Similarity 52.6%;
Matches 10; Conservative
                                                                        Query Match 40.7%;
Best Local Similarity 47.6%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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    SMART; SM00078; IlGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                        RELAXIN (FRAGMENT).
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Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225468D127FE9292 CRC64;
                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
0.29;
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"Characterisation of primate relaxin genes.";
J. Mol. Endocrinol. 0:00(1993).
HSSP; p04090; 6RLX.
33 AA.
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                                                                                                                                                                                                                                                                                                                                    Chung-Sun A., Ji-Tae K., Won-Jin K., Won-Young Y., "Nif-gene organization and nucleotide sequences from Frankia BulKl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Stephanoberyciformes; Cetomimidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21519020; PubMed=11606696;
Miya M., Kawaguchi A., Nishida M.;
"Mitogenomic exploration of higher teleostean phylogenies: A case study for moderate-scale evolutionary genomics with 38 newly determined complete mitochondrial DNA sequences.";
Mol. Biol. Evol. 18:1993-2009(2001).
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    6; Indels
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                                                                                                                                                                                                                  NIFE.
Frankia sp. (strain BuIKI).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Frankineae; Frankia.
                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF119361; AAD17262.1;
InterPro; IPR000318; Nitrogase_compl.
InterPro; IPR000510; Oxidored_nitrognse_1.
Pfam; PF00148; oxidored_nitro; 2.
PROSITE; PS000999; NITROGENASE_1.1; 1.
PROSITE; PS0009090; NITROGENASE_1.2; 1.
SEQUENCE 494 AA; 53478 MW; OC56192C3A567770 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0945S5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 5.
                                                                                                                                  PRT; 494 AA.
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 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.3%; Score 51.5; I Best Local Similarity 50.0%; Pred. No. 12; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                           7 VRLCGREFIRAVIFTCGGS 25
                                           8 IKVCGRELVRVQIAICGMS 26
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9; Conservative
                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                              NCBI_TaxID=47227;
                                                                                                                                                                                                                                                                                                                      STRAIN=EUIK1;
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Q9Z5Y5;
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DR EMBL; AP002936; BAB70258.1; -.

KW Mitochondrion.

SQ SEQUENCE 612 AA; 67303 MW; 3D412F049DAF4907 CRC64;

SQUEDY Match

Query Match

Best Local Similarity 42.1%; Pred. No. 17;

Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps

QY 7 VRLCGREFIRAVIFTCGGS 25

| | | | | | | | | | |
| Db 333 VHICTHAFFRAMLFLCSGS 351

Search completed: June 27, 2002, 16:16:29

Job time: 498 sec
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